

SEQUENCE LISTING

<110> O'Donnell, Michael E.

Yuzhakov, Alexander

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Jeruzalmi, David

Bruck, Irina

Kuriyan, John

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

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<211> 2007

<212> DNA

<213> *Thermus thermophilus*

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Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
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Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
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Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
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Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
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															85
															90

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 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser  
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 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro  
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 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro  
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 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu  
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 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg  
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 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu  
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 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro  
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 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr  
 245 250 255  
  
 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala  
 260 265 270  
  
 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu  
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 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln  
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 370 375 380  
  
 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg  
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 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys  
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 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro  
 420 425 430  
  
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu  
 435 440 445  
  
 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro  
 450 455 460  
  
 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu  
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 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg  
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 Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu  
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<212> PRT

<213> Thermus thermophilus

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Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
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Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
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Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
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Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
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Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu  
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Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser  
115 120 125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro  
130 135 140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro  
145 150 155 160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu  
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Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg  
180 185 190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly  
195 200 205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu  
210 215 220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro  
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Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr  
245 250 255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala  
260 265 270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu  
275 280 285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln  
290 295 300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu  
305 310 315 320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala  
325 330 335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro  
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Ser	Pro	Glu	Val	Gly	Pro	Lys	Pro	Glu	Ser	Pro	Pro	Thr	Pro	Glu	Pro
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370							375							380	
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385							390				395			400	
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<213> Thermus thermophilus

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Met	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
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Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
										25				30	
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
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Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
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Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
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Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser

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Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
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Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
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Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln		
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Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu		
305	310	315
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Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala		
325	330	335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro		

340	345	350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro		
355	360	365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe		
370	375	380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg		
385	390	395
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys		
405	410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro		
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His Ala Tyr Leu Phe Ser Gly Thr		
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<210> 8  
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<210> 9  
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<210> 10  
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<223> Description of Artificial Sequence: primer

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<212> PRT

<213> Escherichia coli

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Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala  
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Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly  
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys  
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg  
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln  
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val  
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln  
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys  
165 170 175

Ala Leu Asp Val  
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<210> 20  
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 <212> PRT  
 <213> *Bacillus subtilis*

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     20                       25                       30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly  
     35                       40                       45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys  
     50                       55                       60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys  
     65                       70                       75                       80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala  
     85                       90                       95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys  
     100                       105                       110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val  
     115                       120                       125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
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Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His  
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Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys  
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Arg Ile Thr Ser  
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<213> Escherichia coli

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20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly  
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys  
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg  
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln  
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val  
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln  
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys  
165 170 175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn  
180 185 190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg  
195 200 205

Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala  
210 215 220

Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met  
225 230 235 240

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met  
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala  
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu  
275 280 285

Leu His Arg Ile Ala Met  
290

<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala  
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu  
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly  
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys  
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys  
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln  
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val  
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln  
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys  
                   165                  170                  175  
  
 Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr  
                   180                  185                  190  
  
 Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys  
                   195                  200                  205  
  
 Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala  
                   210                  215                  220  
  
 Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met  
                   225                  230                  235                  240  
  
 Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu  
                   245                  250                  255  
  
 His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala  
                   260                  265                  270  
  
 Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys  
                   275                  280                  285  
  
 Leu His Gln Ile Ala Leu  
                   290

<210> 23  
 <211> 294  
 <212> PRT  
 <213> Bacillus subtilis

<400> 23  
 Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu  
     1              5                  10                  15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu  
     20                  25                  30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly  
     35                  40                  45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys  
     50                  55                  60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65

70

75

80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala  
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys  
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val  
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His  
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys  
165 170 175

Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp  
180 185 190

Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser  
195 200 205

Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala  
210 215 220

Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile  
225 230 235 240

Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu  
245 250 255

His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu  
260 265 270

Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr  
275 280 285

Phe Arg Asp Met Leu Leu  
290

<210> 24

<211> 300

<212> PRT

<213> Caulobacter crescentus

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu  
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe  
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly  
35 40 45

Val Gly Lys Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr  
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly  
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu  
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu  
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile  
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu  
130 135 140

Lys Thr Leu Glu Glu Pro Pro His Ala Lys Phe Ile Phe Ala Thr  
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg  
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp  
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala  
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu  
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser  
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly	Leu Ala Asp Arg Ser Gln Thr Ile		
245	250	255	
Ala Leu Tyr Glu His Val Met Ala Gly Lys	Thr Lys Asp Ala Leu Glu		
260	265	270	
Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met			
275	280	285	
Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val			
290	295	300	
<210> 25			
<211> 260			
<212> PRT			
<213> Mycoplasma genitalium			
<400> 25			
Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln			
1	5	10	15
Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn			
20	25	30	
Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr			
35	40	45	
Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu			
50	55	60	
Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser			
65	70	75	80
Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser			
85	90	95	
Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn			
100	105	110	
His Pro Phe Thr Phe Lys Lys Val Tyr Ile Leu Asp Glu Ala His			
115	120	125	
Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu			
130	135	140	
Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Glu Phe Asn Lys			
145	150	155	160

Ile	Pro	Leu	Thr	Ile	Leu	Ser	Arg	Cys	Gln	Ser	Phe	Phe	Phe	Lys	Lys
				165					170					175	
Ile	Thr	Ser	Asp	Leu	Ile	Leu	Glu	Arg	Leu	Asn	Asp	Ile	Ala	Lys	Lys
				180					185					190	
Glu	Lys	Ile	Lys	Ile	Glu	Lys	Asp	Ala	Leu	Ile	Lys	Ile	Ala	Asp	Leu
				195				200				205			
Ser	Gln	Gly	Ser	Leu	Arg	Asp	Gly	Leu	Ser	Leu	Leu	Asp	Gln	Leu	Ala
				210				215				220			
Ile	Ser	Leu	Ile	Val	Lys	Lys	Leu	Val	Leu	Leu	Met	Leu	Lys	Lys	His
				225				230			235			240	
Leu	Ile	Ser	Leu	Ile	Glu	Met	Gln	Asn	Leu	Leu	Leu	Leu	Lys	Gln	Phe
				245				250					255		
Tyr	Gln	Glu	Ile												
				260											
<210> 26															
<211> 289															
<212> PRT															
<213> Thermus thermophilus															
<400> 26															
Val	Ser	Ala	Leu	Tyr	Arg	Arg	Phe	Arg	Pro	Leu	Thr	Phe	Gln	Glu	Val
					1				5			10			15
Val	Gly	Gln	Glu	His	Val	Lys	Glu	Pro	Leu	Leu	Lys	Ala	Ile	Arg	Glu
					20				25				30		
Gly	Arg	Leu	Ala	Gln	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly	Val	Gly
					35				40			45			
Lys	Thr	Thr	Thr	Ala	Arg	Leu	Leu	Ala	Met	Ala	Val	Gly	Cys	Gln	Gly
					50				55			60			
Glu	Asp	Pro	Pro	Cys	Gly	Val	Cys	Pro	His	Cys	Gln	Ala	Val	Gln	Arg
					65				70			75			80
Gly	Ala	His	Pro	Asp	Val	Val	Asp	Ile	Asp	Ala	Ala	Ser	Asn	Asn	Ser
					85				90				95		
Val	Glu	Asp	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ile	His	Leu	Ala	Pro	Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
240		
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr		

<210> 27  
 <211> 94  
 <212> DNA  
 <213> Thermus thermophilus

<400> 27  
 gccggaggga gaaaaaaaaa gccgagccca aggccccgcc cggccccacc ccgaagcgcc 60  
 cgaccccccgcg ggccccccga ggaggaggag aggc 94

<210> 28  
<211> 11  
<212> PRT  
<213> Thermus thermophilus

<400> 28  
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro  
1 5 10

<210> 29  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> unsure  
<222> (6)  
<223> N at position 6 is either G or C

<220>  
<221> unsure  
<222> (12)  
<223> N at position 12 is either G or C

<220>  
<221> unsure  
<222> (21)  
<223> N at position 21 is either G or C

<400> 29  
cacgcntacc tnttctccgg nac

23

<210> 30  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<220>  
<221> unsure

<222> (7)  
<223> N at position 7 is either G or C

<220>  
<221> unsure  
<222> (10)  
<223> N at position 10 is either G or C

<220>  
<221> unsure  
<222> (19)  
<223> N at position 19 is either G or C

<220>  
<221> unsure  
<222> (22)  
<223> N at position 22 is either G or C

<400> 30  
gtgctcnggn ggctcctcnt cngtc

25

<210> 31  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 31  
gtgggatccg tggttctgga tctcgatgaa gaa

33

<210> 32  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 32  
gtgggatcca cggsctstcs gagcagaag

29

<210> 33  
<211> 34

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 33  
gcgggatcct caacgaggac ctctccatct tcaa 34

<210> 34  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 34  
gcgggatcct tgtcgtsag sgtsagsgcg tcgta 35

<210> 35  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 35  
ggaaaggacc agcgctact ccccctgctc ctaggtgtg 39

<210> 36  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 36  
gtgtggatcc ttcttcttsc ccatsgc 27

<210> 37  
<211> 27

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 37  
caccgattcc agtgtgcct aggtgtg 27

<210> 38  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 38  
caacacacctgg tttccagga gcctgtgctt 30

<210> 39  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 39  
ccagaatcgt ctgctggtcg tag 23

<210> 40  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 40  
agcacccctgg aggagcttc 19

<210> 41  
<211> 19

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 41  
catgtcgtac tgggtgtac

19

<210> 42  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<220>  
<221> unsure  
<222> (7)  
<223> N at position 7 is A, C, G, or T  
  
<220>  
<221> unsure  
<222> (8)  
<223> N at position 8 is A, C, G, or T  
  
<220>  
<221> unsure  
<222> (13)  
<223> N at position 13 is A, C, G, or T  
  
<220>  
<221> unsure  
<222> (14)  
<223> N at position 14 is A, C, G, or T  
  
<400> 42  
gtsgtsnnsg acnnsgagac sacsggg

27

<210> 43  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctctgtgg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccccttgcg gctccgggtg

30

<210> 46  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 46  
gcgtctaga cgagttccca aagcgtgcgg t 31

<210> 47  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 47  
cggtctaga tcacaccttat ccaga 25

<210> 48  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 48  
gcggcgata tggtggtggt cctggacctg gag 33

<210> 49  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 49  
cggtctaga tcacaccttat ccaga 25

<210> 50  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 50  
gtstctsgtta agacscactt 20

<210> 51  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 51  
sagsagsgcg ttgaasgtgt g 21

<210> 52  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 52  
ctcgttggtg aaagttccg tg 22

<210> 53  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 53  
ctcgttggtg aaagttccg tg 22

<210> 54  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 54  
tctggcaaca cgttctggag cacatcc 27

<210> 55  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 55  
tgctggcggtt catcttcagg atg 23

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 56  
catcctgaag atgaacgcca gca 23

<210> 57  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 57  
aggtttatcca caggggtcat gtgca 25

<210> 58  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 58  
gtgtgtcata tgaacataaac ggttcccaa 29

<210> 59  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 59  
gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60  
<211> 13  
<212> PRT  
<213> Thermus thermophilus

<400> 60  
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp  
1 5 10

<210> 61  
<211> 14  
<212> PRT  
<213> Thermus thermophilus

<400> 61  
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys  
1 5 10

<210> 62  
<211> 8

<212> PRT  
<213> Thermus thermophilus

<400> 62  
Phe Phe Ile Glu Ile Gln Asn His  
1 5

<210> 63  
<211> 8  
<212> PRT  
<213> Thermus thermophilus

<400> 63.  
Tyr Asp Ala Leu Thr Leu Asp Asp  
1 5

<210> 64  
<211> 6  
<212> PRT  
<213> Thermus thermophilus

<400> 64  
Ala Met Gly Lys Lys Lys  
1 5

<210> 65  
<211> 9  
<212> PRT  
<213> Thermus thermophilus

<400> 65  
Phe Asn Lys Ser His Ser Ala Ala Tyr  
1 5

<210> 66  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE

<222> (3)  
<223> Xaa at position 3 is undefined

<220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at position 5 is undefined

<400> 66  
Val Val Xaa Asp Xaa Glu Thr Thr Gly  
1 5

<210> 67  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE  
<222> (4)  
<223> Xaa at position 4 is undefined

<220>  
<221> PEPTIDE  
<222> (7)  
<223> Xaa at position 7 is undefined

<400> 67  
His Asn Ala Xaa Phe Asp Xaa Gly Phe  
1 5

<210> 68  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<220>  
<221> PEPTIDE  
<222> (3)  
<223> Xaa at position 3 is undefined

<220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at position 5 is undefined

<400> 68  
Val Val Xaa Asp Xaa Glu Thr Thr Gly  
1 5

<210> 69  
<211> 7  
<212> PRT  
<213> Thermus thermophilus

<400> 69  
Val Leu Val Lys Thr His Leu  
1 5

<210> 70  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: peptide

<400> 70  
His Arg Ala Leu Tyr Asp  
1 5

<210> 71  
<211> 7  
<212> PRT  
<213> Thermus thermophilus

<400> 71  
His Thr Phe Asn Ala Leu Leu  
1 5

<210> 72  
<211> 34  
<212> PRT  
<213> Escherichia coli

<400> 72  
Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu  
1 5 10 15  
  
Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro  
20 25 30  
  
Val Val

<210> 73  
<211> 34  
<212> PRT  
<213> Vibrio cholerae  
  
<400> 73  
Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu  
1 5 10 15  
  
Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro  
20 25 30  
  
Val Val

<210> 74  
<211> 34  
<212> PRT  
<213> Haemophilus influenzae  
  
<400> 74  
Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu  
1 5 10 15  
  
Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro  
20 25 30  
  
Leu Val

<210> 75  
<211> 34  
<212> PRT  
<213> Rickettsia prowazekii

<400> 75  
Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln  
1 5 10 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro  
20 25 30

Ile Val

<210> 76  
<211> 34  
<212> PRT  
<213> Helicobacter pylori

<400> 76  
Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg  
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys  
20 25 30

Ile Ile

<210> 77  
<211> 34  
<212> PRT  
<213> Synechocystis sp.

<400> 77  
Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg  
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys  
20 25 30

Ile Val

<210> 78  
<211> 34  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 78  
Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg  
1 5 10 15  
  
Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro  
20 25 30  
  
Pro Leu

<210> 79  
<211> 46  
<212> PRT  
<213> Escherichia coli

<400> 79  
Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala  
1 5 10 15  
  
Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu  
20 25 30  
  
Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp  
35 40 45

<210> 80  
<211> 46  
<212> PRT  
<213> Vibrio cholerae

<400> 80  
Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala  
1 5 10 15  
  
Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys  
20 25 30  
  
Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu  
35 40 45

<210> 81  
<211> 46  
<212> PRT  
<213> Haemophilus influenzae

<400> 81  
Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala  
1 5 10 15  
  
Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu  
20 25 30  
  
Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp  
35 40 45

<210> 82  
<211> 46  
<212> PRT  
<213> Rickettsia prowazekii

<400> 82  
Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp  
1 5 10 15  
  
Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys  
20 25 30  
  
Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp  
35 40 45

<210> 83  
<211> 45  
<212> PRT  
<213> Helicobacter pylori

<400> 83  
Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser  
1 5 10 15  
  
Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp  
20 25 30  
  
Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln  
35 40 45

<210> 84  
<211> 46  
<212> PRT  
<213> Synechocystis sp.

<210> 85  
<211> 46  
<212> PRT  
<213> *Mycobacterium tuberculosis*

```

<400> 85
Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
      1           5           10          15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
      20          25          30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
      35          40          45

```

<210> 86  
<211> 3729  
<212> DNA  
<213> *Thermus thermophilus*

<400> 86  
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ggggcgcgca agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120  
gccttgccca tgaccgacca cggcaacctc ttccgggccc tggagttcta caagaaggcc 180  
accgaaatgg gcatcaagcc catcctggc tacgaggcct acgtggcggc ggaaaaggccg 240  
tttgaccgca agcggggaaa gggcctagac gggggctact ttcacacctac cctcctcgcc 300  
aaggacttca cggggtacca gaacctggtg cgcctggcga gcccggctta cctggagggg 360  
ttttacgaaa agccccggat tgaccggag atcctgcgcg agcacgccc gggcctcatc 420  
gcctctcgg ggtgcctcgg ggcggagatc ccccagttca tcctccagga ccgtctggac 480  
ctggccgagg cccggctcaa cgagtacctc tccatcttca aggaccgctt cttcatcgag 540  
atccagaacc acggcctccc cgagcagaaa aaggtcaacg aggtcctcaa ggagttcgcc 600  
cgaaaagtacg gcctggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660  
gccccgcggcc acgaggtccat cctcgccatc cagtccaaga gcaccctgga cgaccgggg 720  
cgctggcgct tccccctgcga cgagttctac gtgaagaccc ccgaggagat gcggggccatg 780  
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tgcaacgtgg agctgccccat cggggacaag atggcttacc gaatcccccg cttccccctc 900  
cccgaggggc ggaccgaggc ccagtacccctc atggagctca ccttcaggg gctccctccgc 960  
cgctacccgg accggatcac cgagggcttc taccgggagg tcttccgcct tttggggaaag 1020  
cttccccccc acggggacgg ggaggccttgc cccgaggcct tggcccaaggt ggagcgggag 1080  
gcttgggaga ggctcatgaa gagcctcccc ccttggccg ggtcaagga gtggacggcg 1140  
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ggctacttcc tcatacgccca ggactacatc aactggccc ggagaaacgg cgtctccgt 1260  
ggggccggca gggggagcgc cgccgggagc ctggggcct acggcggtgg gatcaccaac 1320  
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atgcccggaca ttgacacggc cttctccgac cgggagcggg accgggtgat ccagtacg 1440  
cgggagcgt acggcgagga caagggtggcc cagatcgca ccctggaaag cctccctcc 1500  
aaggccgccc tcaaggacgt ggcccggtc tacggcatcc cccacaagaa ggccggaggaa 1560  
ttggccaagc tcatacccggt gcagttcggg aagcccaagc ccctgcagga gccatccag 1620  
gtgggtccgg agcttagggc ggagatggag aaggacccca aggtgcgggaa ggtcctcgag 1680  
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gtggagctgg actacgatgc cctcccccgt gacgacccca agaccttcgc cctccctctcc 1980  
cggggggaga ccaagggggt cttccagctg gagtcggggg ggatgaccgc cacgctccgc 2040  
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gaggcggacc tcctcgccg gtccatgggc aagaagaagg tggaggagat gaagtccac 2340  
cgggagcgt tcgtccaggg ggccaaggaa agggcggtgc ccgaggagga ggccaaccgc 2400  
ctcttgcaca tgctggggc cttcgccaaac tacggcttca acaaatccca cgctgccg 2460  
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gcccccctcc tctccgttga gcccacgac tccgacaagg tggccgagta catccgcac 2580  
gcccggccca tgggcatacgaa ggtccttccc ccggacgtca accgctccgg gtttgacttc 2640  
ctgggtccagg gcccggagat cctttcgcc ctctccgccc tgaagaacgt gggcgaggcg 2700  
gcggcggagg ccattctccg ggagcggggag cggggcgcc cctaccggag cctccggc 2760  
ttccctcaagc ggctggacga gaaggtgctc aacaagcgaa ccctggagtc cctcatcaag 2820  
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ctcaagtggg cggccggagaa ccgggagaag gcccgtccg gcatgtatggg cctcttcage 2940  
gaagtggagg agccgcctt ggccgaggcc gccccctgg acgagatcac ccggctccgc 3000  
tacgagaagg agggccctgg gatctacgtc tccgcccacc ccatttgcgt gtaccccccgg 3060  
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ccccggctca gggccttccct tgccggatg gtggaggagg tggtgcgaa gcccacaag 3180  
agcggcgaaa tgatggccc cttcgccctc tccgacgaga cggggggcgct tgaggcggtg 3240  
gcattcgccg gggcctacga ccaggctcc ccgaggctca aggaggacac cccctgtc 3300  
gtcctcgccg aggtggagcg ggaggagggg ggcgtgcggg tgctggccca ggccgtttgg 3360  
acctacgagg agctggagca ggtccccccgg gcccgtccagg tggaggtggaa ggcctccctc 3420  
ctggacgacc ggggggtggc ccacctgaaa agccttctgg acgagacacgc ggggaccctc 3480  
cccctgtacg tccgggtcca gggcgccttc ggcgaggccc tccctccctt gagggggtg 3540  
cggggtgggg aggaggctgt aggccggccgc gtgggtccgg gcctacccctc tgcccggaccg 3600  
ggaggtccctt ctccaggccg gccaggccgg ggaggcccag gaggcggtgc cttcttaggg 3660  
ggtggccgt gagacccatgc gccatcgatc tcggccgggg caaggaggcc tggggccgac 3720

ccctttgg

3729

<210> 87  
<211> 1245  
<212> PRT  
<213> Thermus thermophilus

<400> 87  
Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe  
1 5 10 15  
  
Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val  
20 25 30  
  
Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly  
35 40 45  
  
Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly  
50 55 60  
  
Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg  
65 70 75 80  
  
Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu  
85 90 95  
  
Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu  
100 105 110  
  
Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp  
115 120 125  
  
Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly  
130 135 140  
  
Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp  
145 150 155 160  
  
Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg  
165 170 175  
  
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val  
180 185 190  
  
Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val  
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His  
210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly  
225 230 235 240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu  
245 250 255

Met Arg Ala Met Phe Pro Glu Glu Val Gly Gly Arg Ser Pro Leu  
260 265 270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly  
275 280 285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg  
290 295 300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg  
305 310 315 320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg  
325 330 335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu  
340 345 350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser  
355 360 365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe  
370 375 380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro  
385 390 395 400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys  
405 410 415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val  
420 425 430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu  
435 440 445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile  
450 455 460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val  
465 470 475 480

Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly  
485 490 495

Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly  
500 505 510

Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln  
515 520 525

Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu  
530 535 540

Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu  
545 550 555 560

Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala  
565 570 575

Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu  
580 585 590

Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala  
595 600 605

Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr  
610 615 620

Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly  
625 630 635 640

Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe  
645 650 655

Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser  
660 665 670

Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu  
675 680 685

Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His  
690 695 700

Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr  
705 710 715 720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu  
 725 730 735  
  
 Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser  
 740 745 750  
  
 Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser  
 755 760 765  
  
 Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe  
 770 775 780  
  
 Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Ala Asn Arg  
 785 790 800  
  
 Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser  
 805 810 815  
  
 His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys  
 820 825 830  
  
 Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg  
 835 840 845  
  
 His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met  
 850 855 860  
  
 Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe  
 865 870 880  
  
 Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn  
 885 890 895  
  
 Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly  
 900 905 910  
  
 Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys  
 915 920 925  
  
 Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu  
 930 935 940  
  
 Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu  
 945 950 955 960  
  
 Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met  
 965 970 975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro  
980 985 990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile  
995 1000 1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr  
1010 1015 1020

Ala Thr Cys Thr Leu Glu Leu Pro His Leu Ala Arg Asp Leu Pro  
1025 1030 1035 1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg  
1045 1050 1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp  
1060 1065 1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln  
1075 1080 1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu  
1090 1095 1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp  
1105 1110 1115 1120

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val  
1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu  
1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly  
1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu  
1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu  
1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg  
1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala  
1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu  
1235                            1240                            1245

<210> 88  
<211> 198  
<212> PRT  
<213> Thermus thermophilus

<400> 88  
Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu  
1                                5                                10                            15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly  
20                              25                                30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu  
35                              40                                45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg  
50                              55                                60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg  
65                              70                                75                            80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro  
85                              90                                95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala  
100                            105                                110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro  
115                            120                                125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser  
130                            135                                140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu  
145                            150                                160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg  
165                            170                                175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr  
180                            185                                190

Tyr Met Leu Thr Ser Gly  
195

<210> 89  
 <211> 182  
 <212> PRT  
 <213> Deinococcus radiodurans

<220>  
 <221> PEPTIDE  
 <222> (79)  
 <223> X at position 79 is undefined

<400> 89  
 Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe  
     1               5                   10                   15

Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val  
     20                   25                   30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro  
     35                   40                   45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg  
     50                   55                   60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys  
     65                   70                   75                   80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val  
     85                   90                   95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu  
     100                   105                   110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln  
     115                   120                   125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val  
     130                   135                   140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg  
     145                   150                   155                   160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu  
     165                   170                   175

Glu Leu Leu Gly Glu Arg  
     180

<210> 90  
<211> 201  
<212> PRT  
<213> Bacillus subtilis

<400> 90  
His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp  
1 5 10 15  
  
Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu  
20 25 30  
  
Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr  
35 40 45  
  
Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile  
50 55 60  
  
Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala  
65 70 75 80  
  
Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala  
85 90 95  
  
Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp  
100 105 110  
  
Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn  
115 120 125  
  
Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val  
130 135 140  
  
Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn  
145 150 155 160  
  
His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln  
165 170 175  
  
His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu  
180 185 190  
  
Lys Met Leu Lys Asp Ala Ala Glu Lys  
195 200

<210> 91  
<211> 188  
<212> PRT  
<213> Haemophilus influenzae

<220>  
<221> PEPTIDE  
<222> (47)  
<223> X at position 47 is undefined

<220>  
<221> PEPTIDE  
<222> (57)  
<223> X at position 57 is undefined

<400> 91  
Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly  
1 5 10 15  
  
Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile  
20 25 30  
  
Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His  
35 40 45  
  
Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val  
50 55 60  
  
His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu  
65 70 75 80  
  
Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile  
85 90 95  
  
His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys  
100 105 110  
  
Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr  
115 120 125  
  
Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp  
130 135 140  
  
Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His  
145 150 155 160  
  
Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met  
165 170 175

Thr	Gly	Gly	Gln	Thr	Asn	Leu	Phe	Asp	Glu	Glu	Glu				
				180				185							
<210> 92															
<211> 189															
<212> PRT															
<213> Escherichia coli															
<400> 92															
Met	Ser	Thr	Ala	Ile	Thr	Arg	Gln	Ile	Val	Leu	Asp	Thr	Glu	Thr	Thr
1				5				10				15			
Gly	Met	Asn	Gln	Ile	Gly	Ala	His	Ser	Glu	Gly	His	Lys	Ile	Ile	Glu
	20						25					30			
Ile	Gly	Ala	Val	Glu	Val	Val	Asn	Arg	Arg	Leu	Thr	Gly	Asn	Asn	Phe
	35						40				45				
His	Val	Tyr	Leu	Lys	Asp	Arg	Leu	Val	Asp	Pro	Glu	Ala	Phe	Gly	Val
	50				55				60						
His	Gly	Ile	Ala	Val	Asp	Phe	Leu	Leu	Asp	Lys	Pro	Thr	Phe	Ala	Glu
	65				70				75				80		
Val	Ala	Val	Glu	Phe	Met	Asp	Tyr	Ile	Arg	Gly	Ala	Glu	Leu	Val	Ile
			85					90				95			
His	Asn	Ala	Ala	Phe	Asp	Ile	Gly	Phe	Met	Asp	Tyr	Glu	Phe	Ser	Leu
	100					105				110					
Leu	Lys	Arg	Asp	Ile	Ala	Lys	Thr	Asn	Thr	Phe	Cys	Lys	Val	Thr	Asp
	115					120				125					
Ser	Leu	Ala	Val	Ala	Arg	Lys	Met	Phe	Pro	Gly	Lys	Arg	Asn	Ser	Leu
	130				135				140						
Asp	Ala	Leu	Cys	Ala	Arg	Tyr	Glu	Ile	Asp	Asn	Ser	Lys	Arg	Thr	Leu
	145				150				155			160			
His	Gly	Ala	Leu	Leu	Asp	Ala	Gln	Ile	Leu	Ala	Glu	Val	Tyr	Leu	Ala
			165					170				175			
Met	Thr	Gly	Gly	Gln	Thr	Ser	Met	Ala	Phe	Ala	Met	Glu			
					180			185							

<210> 93  
<211> 201  
<212> PRT  
<213> Helicobacter pylori

<400> 93

Asn	Leu	Glu	Tyr	Leu	Lys	Ala	Cys	Gly	Leu	Asn	Phe	Ile	Glu	Thr	Ser
1		5							10					15	
Glu	Asn	Leu	Ile	Thr	Leu	Lys	Asn	Leu	Lys	Thr	Pro	Leu	Lys	Asp	Glu
	20				25								30		
Val	Phe	Ser	Phe	Ile	Asp	Leu	Glu	Thr	Thr	Gly	Ser	Cys	Pro	Ile	Lys
	35				40						45				
His	Glu	Ile	Leu	Glu	Ile	Gly	Ala	Val	Gln	Val	Lys	Gly	Gly	Glu	Ile
	50				55					60					
Ile	Asn	Arg	Phe	Glu	Thr	Leu	Val	Lys	Val	Lys	Ser	Val	Pro	Asp	Tyr
	65			70				75					80		
Ile	Ala	Glu	Leu	Thr	Gly	Ile	Thr	Tyr	Glu	Asp	Thr	Leu	Asn	Ala	Pro
	85				90						95				
Ser	Ala	His	Glu	Ala	Leu	Gln	Glu	Leu	Arg	Leu	Phe	Leu	Gly	Asn	Ser
	100				105					110					
Val	Phe	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr	Asn	Phe	Leu	Gly	Arg
	115				120					125					
Tyr	Phe	Val	Glu	Lys	Leu	His	Cys	Pro	Leu	Leu	Asn	Leu	Lys	Leu	Cys
	130			135						140					
Thr	Leu	Asp	Leu	Ser	Lys	Arg	Ala	Ile	Leu	Ser	Met	Arg	Tyr	Ser	Leu
	145			150				155				160			
Ser	Phe	Leu	Lys	Glu	Leu	Leu	Gly	Phe	Gly	Ile	Glu	Val	Ser	His	Arg
	165				170					175					
Ala	Tyr	Ala	Asp	Ala	Leu	Ala	Ser	Tyr	Lys	Leu	Phe	Glu	Ile	Cys	Leu
	180				185					190					
Leu	Asn	Leu	Pro	Ser	Tyr	Ile	Lys	Thr							
	195			200											

<210> 94  
<211> 630

<212> DNA

<213> Thermus thermophilus

<400> 94

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ctggagacca cggggcgttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180  
gagggggggga ggcgcctccc ctccagagc ctcgtccggc ccctcccgc cgccgaagcc 240  
cgtcgtgga acctcaccgg catccccgg gaggccctgg aggaggcccc ctccctggag 300  
gaggttctgg agaaggccta ccccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360  
gcctttgacc tgggcttcct ccccccggc ttggaggggc tgggctaccg cctggaaaaac 420  
cccggtggtgg actccctgca cttggccaga cggggcttac caggccttag gcgtacggc 480  
ctggacgccc tctccgaggt cctggagctt ccccgaaagga cctgcccacccg ggcctcgag 540  
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cccgcacgc tttgggaact cgggaggtag 630

<210> 95

<211> 210

<212> PRT

<213> Thermus thermophilus

<400> 95

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu  
1 5 10 15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu  
20 25 30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly  
35 40 45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg  
50 55 60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala  
65 70 75 80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala  
85 90 95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp  
100 105 110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg  
115 120 125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp

130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
165	170	175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
180	185	190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
195	200	205
Arg Glx		
210		
<210> 96		
<211> 461		
<212> PRT		
<213> Pseudomonas marcesans		
<400> 96		
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn		
1	5	10
15		
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser		
20	25	30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser		
35	40	45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala		
50	55	60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala		
65	70	75
80		
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro		
85	90	95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu		
100	105	110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe		
115	120	125

Asn Arg Phe Val Val Gly Pro Asn Ser Arg Met Ala His Ala Ala Ala  
130 135 140

Met Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe Ile  
145 150 155 160

Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile Gly  
165 170 175

His Tyr Arg Leu Glu Ile Asp Pro Gly Ala Lys Val Ser Tyr Val Ser  
180 185 190

Thr Glu Thr Phe Thr Asn Asp Leu Ile Leu Ala Ile Arg Gln Asp Arg  
195 200 205

Met Gln Ala Phe Arg Asp Arg Tyr Arg Ala Ala Asp Leu Ile Leu Val  
210 215 220

Asp Asp Ile Gln Phe Ile Glu Gly Lys Glu Tyr Thr Gln Glu Glu Phe  
225 230 235 240

Phe His Thr Phe Asn Ala Leu His Asp Ala Gly Ser Gln Ile Val Leu  
245 250 255

Ala Ser Asp Arg Pro Pro Ser Gln Ile Pro Arg Leu Gln Glu Arg Leu  
260 265 270

Met Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Val Gln Ala Pro Asp  
275 280 285

Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu His Glu Arg  
290 295 300

Val Gly Leu Pro Arg Asp Leu Ile Gln Phe Ile Ala Gly Arg Phe Thr  
305 310 315 320

Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Thr Arg Ala Ile Ala Phe  
325 330 335

Ala Ser Ile Thr Gly Leu Pro Met Thr Val Asp Ser Ile Ala Pro Met  
340 345 350

Leu Asp Pro Asn Gly Gln Gly Val Glu Val Thr Pro Lys Gln Val Leu  
355 360 365

Asp Lys Val Ala Glu Val Phe Lys Val Thr Pro Asp Glu Met Arg Ser  
370 375 380

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr  
385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr  
405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val  
420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys  
435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg  
450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala  
1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val  
20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly  
35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu  
50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr  
65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro  
85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr  
100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala  
115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe  
130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile  
 145 150 155 160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val  
 165 170 175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp  
 180 185 190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu  
 195 200 205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu  
 210 215 220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val  
 225 230 235 240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg  
 245 250 255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro  
 260 265 270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp  
 275 280 285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr  
 290 295 300

Thr Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Ala Ile Ala  
 305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro  
 325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile  
 340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu  
 355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met  
 370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu  
 385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys  
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr  
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser  
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu  
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys  
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu  
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp  
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile  
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys  
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn  
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe  
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr  
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu  
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

165	170	175
Val Val Tyr Leu Ser Ser Glu Lys Phe Thr Asn Glu Phe Ile Asn Ser		
180	185	190
Ile Arg Asp Asn Lys Ala Val Asp Phe Arg Asn Arg Tyr Arg Asn Val		
195	200	205
Asp Val Leu Leu Ile Asp Asp Ile Gln Phe Leu Ala Gly Lys Glu Gln		
210	215	220
Thr Gln Glu Glu Phe Phe His Thr Phe Asn Thr Leu His Glu Glu Ser		
225	230	235
Lys Gln Ile Val Ile Ser Ser Asp Arg Pro Pro Lys Glu Ile Pro Thr		
245	250	255
Leu Glu Asp Arg Leu Arg Ser Arg Phe Glu Trp Gly Leu Ile Thr Asp		
260	265	270
Ile Thr Pro Pro Asp Leu Glu Thr Arg Ile Ala Ile Leu Arg Lys Lys		
275	280	285
Ala Lys Ala Glu Gly Leu Asp Ile Pro Asn Glu Val Met Leu Tyr Ile		
290	295	300
Ala Asn Gln Ile Asp Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Ile		
305	310	315
Arg Val Val Ala Tyr Ser Ser Leu Ile Asn Lys Asp Ile Asn Ala Asp		
325	330	335
Leu Ala Ala Glu Ala Leu Lys Asp Ile Ile Pro Ser Ser Lys Pro Lys		
340	345	350
Val Ile Thr Ile Lys Glu Ile Gln Arg Val Val Gly Gln Gln Phe Asn		
355	360	365
Ile Lys Leu Glu Asp Phe Lys Ala Lys Lys Arg Thr Lys Ser Val Ala		
370	375	380
Phe Pro Arg Gln Ile Ala Met Tyr Leu Ser Arg Glu Met Thr Asp Ser		
385	390	395
400		
Ser Leu Pro Lys Ile Gly Glu Glu Phe Gly Gly Arg Asp His Thr Thr		
405	410	415
Val Ile His Ala His Glu Lys Ile Ser Lys Leu Leu Ala Asp Asp Glu		

420 425 430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys  
435 440 445

<210> 99  
<211> 507  
<212> PRT  
<213> Mycobacterium tuberculosis

<400> 99  
Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val  
1 5 10 15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser  
20 25 30

Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu  
35 40 45

Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser  
50 55 60

Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala  
65 70 75 80

Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu  
85 90 95

Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr  
100 105 110

Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr  
115 120 125

Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Arg Gly Asp Asn Gln  
130 135 140

His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser  
145 150 155 160

Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr  
165 170 175

Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Leu Ala  
180 185 190

Ile	Ala	Glu	Ala	Pro	Ala	Arg	Ala	Tyr	Asn	Pro	Leu	Phe	Ile	Trp	Gly
195															205
Glu	Ser	Gly	Leu	Gly	Lys	Thr	His	Leu	Leu	His	Ala	Ala	Gly	Asn	Tyr
210															220
Ala	Gln	Arg	Leu	Phe	Pro	Gly	Met	Arg	Val	Lys	Tyr	Val	Ser	Thr	Glu
225															240
Glu	Phe	Thr	Asn	Asp	Phe	Ile	Asn	Ser	Leu	Arg	Asp	Asp	Arg	Lys	Val
245															255
Ala	Phe	Lys	Arg	Ser	Tyr	Arg	Asp	Val	Asp	Val	Leu	Leu	Val	Asp	Asp
260															270
Ile	Gln	Phe	Ile	Glu	Gly	Lys	Glu	Gly	Ile	Gln	Glu	Glu	Phe	Phe	His
275															285
Thr	Phe	Asn	Thr	Leu	His	Asn	Ala	Asn	Lys	Gln	Ile	Val	Ile	Ser	Ser
290															300
Asp	Arg	Pro	Pro	Lys	Gln	Leu	Ala	Thr	Leu	Glu	Asp	Arg	Leu	Arg	Thr
305															320
Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	Val	Gln	Pro	Pro	Glu	Leu	Glu
325															335
Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	Ala	Gln	Met	Glu	Arg	Leu	Ala
340															350
Val	Pro	Asp	Asp	Val	Leu	Glu	Leu	Ile	Ala	Ser	Ser	Ile	Glu	Arg	Asn
355															365
Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Val	Thr	Ala	Phe	Ala	Ser
370															380
Leu	Asn	Lys	Thr	Pro	Ile	Asp	Lys	Ala	Leu	Ala	Glu	Ile	Val	Leu	Arg
385															400
Asp	Leu	Ile	Ala	Asp	Ala	Asn	Thr	Met	Gln	Ile	Ser	Ala	Ala	Thr	Ile
405															415
Met	Ala	Ala	Thr	Ala	Glu	Tyr	Phe	Asp	Thr	Thr	Val	Glu	Glu	Leu	Arg
420															430
Gly	Pro	Gly	Lys	Thr	Arg	Ala	Leu	Ala	Gln	Ser	Arg	Gln	Ile	Ala	Met
435															445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln  
450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile  
465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu  
485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg  
500 505

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg  
1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro  
20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe  
35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly  
50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val  
65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro  
85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly  
100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser  
115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Arg Gly Leu  
130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg  
145 150 155 160

Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn
165								170							175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg															
									185						190
180															
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe															
									200						205
195															
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn															
									215						220
210															
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro															
									230						240
225															
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu															
									245						255
240															
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile															
									260						270
255															
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp															
									275						285
270															
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp															
									290						295
285															300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val															
									305						310
300															315
315															
320															
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro															
									325						330
320															335
335															
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly															
									340						345
335															350
350															
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys															
									355						360
350															365
365															
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu															
									370						375
365															380
380															
Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg															
									385						390
380															395
395															
400															
Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala															
									405						410
400															415
415															

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu  
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly  
435 440 445

<210> 101  
<211> 467  
<212> PRT  
<213> Escherichia coli

<400> 101  
Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu  
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu  
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu  
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr  
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr  
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala  
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser  
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr  
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly  
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn  
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu  
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

180	185	190
Lys Pro Asn Ala Lys Val Val	Tyr Met His Ser Glu Arg Phe Val Gln	
195	200	205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg		
210	215	220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe		
225	230	235
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala		
245	250	255
Leu Leu Glu Gly Asn Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro		
260	265	270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp		
275	280	285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala		
290	295	300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu		
305	310	315
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu		
325	330	335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg		
340	345	350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala		
355	360	365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala		
370	375	380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser		
385	390	395
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu		
405	410	415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg		
420	425	430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg		

435

440

445

Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr  
450 455 460

Leu Ser Ser  
465

<210> 102  
<211> 440  
<212> PRT  
<213> Thermatoga maritima

<400> 102  
Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys  
1 5 10 15

Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly  
20 25 30

Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu  
35 40 45

Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu  
50 55 60

Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His  
65 70 75 80

Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr  
85 90 95

Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly  
100 105 110

Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly  
115 120 125

Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Val Gly Leu Gly Lys Thr  
130 135 140

His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp  
145 150 155 160

Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val  
165 170 175

Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg
		180				185						190			
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly
	195				200						205				
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His
	210			215						220					
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys
	225			230				235			240				
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu
	245				250					255					
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala
	260				265					270					
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu
	275				280				285						
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly
	290				295				300						
Ala	Ile	Ile	Lys	Leu	Leu	Val	Tyr	Lys	Glu	Thr	Thr	Gly	Lys	Glu	Val
	305			310				315			320				
Asp	Leu	Lys	Glu	Ala	Ile	Leu	Leu	Lys	Asp	Phe	Ile	Lys	Pro	Asn	
	325				330					335					
Arg	Val	Lys	Ala	Met	Asp	Pro	Ile	Asp	Glu	Leu	Ile	Glu	Ile	Val	Ala
	340				345					350					
Lys	Val	Thr	Gly	Val	Pro	Arg	Glu	Glu	Ile	Leu	Ser	Asn	Ser	Arg	Asn
	355				360				365						
Val	Lys	Ala	Leu	Thr	Ala	Arg	Arg	Ile	Gly	Met	Tyr	Val	Ala	Lys	Asn
	370				375				380						
Tyr	Leu	Lys	Ser	Ser	Leu	Arg	Thr	Ile	Ala	Glu	Lys	Phe	Asn	Arg	Ser
	385				390				395			400			
His	Pro	Val	Val	Val	Asp	Ser	Val	Lys	Lys	Val	Lys	Asp	Ser	Leu	Leu
		405				410					415				
Lys	Gly	Asn	Lys	Gln	Leu	Lys	Ala	Leu	Ile	Asp	Glu	Val	Ile	Gly	Glu
		420				425				430					

Ile Ser Arg Arg Ala Leu Ser Gly  
435 440

<210> 103  
<211> 457  
<212> PRT  
<213> Helicobacter pylori

<400> 103  
Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys  
1 5 10 15  
  
Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln  
20 25 30  
  
Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr  
35 40 45  
  
Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala  
50 55 60  
  
Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala  
65 70 75 80  
  
His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn  
85 90 95  
  
Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp  
100 105 110  
  
Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val  
115 120 125  
  
Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn  
130 135 140  
  
Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu  
145 150 155 160  
  
Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu  
165 170 175  
  
Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn  
180 185 190  
  
Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe  
195 200 205

Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu  
210 215 220

Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile  
225 230 235 240

Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp  
245 250 255

Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro  
260 265 270

Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu  
275 280 285

Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His  
290 295 300

Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser  
305 310 315 320

Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys  
325 330 335

Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu  
340 345 350

Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser  
355 360 365

Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys  
370 375 380

Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser  
385 390 395 400

Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met  
405 410 415

Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Lys Ser Pro Phe Val  
420 425 430

Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp  
435 440 445

Lys Lys Thr Ala Phe Asn Ser Ser Glu  
450 455

<210> 104  
<211> 1305  
<212> DNA  
<213> Thermus thermophilus

<400> 104  
gtgtcgacg aggccgtctg gcaacacgtt ctggagcaca tccgcccgcag catcacccgag 60  
gtggagttcc acacaccttgg ttgaaaggatc cgccccttgg ggatccggga cggggtgctg 120  
gagctcgccg tgccccaccc tcgttgcctg gactggatcc ggcgccacta cgccggcctc 180  
atccaggagg gcccctcggtt cctcggggcc cagggccccg ggtttgagct ccgggtggtg 240  
cccggggtcg tagtccagga ggacatcttc cagccccccgc cgagccccccgg ggcggcaagct 300  
caacccgaag ataccttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360  
ggccgcgtgg ccgtggccga gtccccccggc cgggccttaca acccccttcatctacggg 420  
ggccgtggcc tggaaagac ctacctgatg cacggcgtgg gcccactccg tgcaagcgc 480  
ttccccccaca ttagattaga gtacgtttcc acggaaactt tcaccaacga gctcatcaac 540  
cgcccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggaccc 600  
ctgtgtgtgg acgacgtcca gttcatcgcc ggaaaggagc gcacccagga ggagtttttc 660  
cacacccatca acgcccatttacgaggccac aagcagatca tcctctccctc cgaccggccg 720  
cccaaggaca tcctcaccct ggaggcgcgc ctgcggagcc gctttgagtg gggcctgatc 780  
accgacaatc cagccccca cctggaaacc cggatcgcca tcctgaagat gaacgccagc 840  
agcgggcctg agatccccga ggacgcccctg gatgacatcg cccggcaggt cacctccaaac 900  
atccgggagt gggaaagggc cctcatgcgg gcatcgccct tcgcctccct caacggcggt 960  
gagctgaccc ggcgcgtggc ggccaaggct ctccgacatc ttgcctccag ggagctggag 1020  
gcggaccctt tggagatcat ccgcaaagcg gcgggaccag ttgcgcctga aaccccgaaa 1080  
ggagctcacg gggagcgccg caagaaggag gtggccctcc cccggcagct cgccatgtac 1140  
ctggcgtggg agctcccccc ggcctccctg cccgagatcg accagctcaa cgacgaccgg 1200  
gaccacacca cggccatctca cgccatccag aaggccagg agctcgccga aagcgaccgg 1260  
gaggtgcagg gcctccctccg caccctccgg gaggcgtgca catga 1305

<210> 105  
<211> 434  
<212> PRT  
<213> Thermus thermophilus

<400> 105  
Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg  
1 5 10 15  
  
Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro  
20 25 30  
  
Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe  
35 40 45  
  
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly

50	55	60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val		
65	70	75
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro		
85	90	95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly		
100	105	110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser		
115	120	125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu		
130	135	140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg		
145	150	155
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn		
165	170	175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg		
180	185	190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe		
195	200	205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn		
210	215	220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro		
225	230	235
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu		
245	250	255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile		
260	265	270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp		
275	280	285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp		
290	295	300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val		

305	310	315	320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro			
325		330	335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly			
340	345	350	
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys			
355	360	365	
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu			
370	375	380	
Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg			
385	390	395	400
Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala			
405	410	415	
Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala			
420	425	430	
Cys Thr			

<210> 106  
 <211> 1128  
 <212> DNA  
 <213> Thermus thermophilus

<400> 106  
 atgaacataa cggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcatc 60  
 gtccccctcta gaagcgccaa ccccctctac acctacctgg ggctttacgc cgaggaaggg 120  
 gccttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180  
 gccaaagcc ttccccgggt gctcgtcccc gcccagccct tcttccagct ggtgcggagc 240  
 ctccctgggg acctcgtggc cctcggcctc gcctcggagc cgggccaggg gggcagctg 300  
 gagctctcct ccgggcgttt cccgcacccgg ctcagcctgg cccctgccc gggctacccc 360  
 gagttctgg tgcccgaggg ggaggacaag ggggccttcc ccctccggac gcggatgccc 420  
 tccggggagc tcgtcaaggc cttgacccac gtgcgtacg ccgcgagcaa cgaggagtac 480  
 cggccatct tccgcggggt gcagctggag ttctcccccc agggcttccg ggcggtgccc 540  
 tccgacgggt accgcctcgc cctctacgac ctgcccctgc cccaagggtt ccaggccaag 600  
 gccgtggtcc ccgccccggag cgtggacgag atgggtgcggg tcctgaaggg ggcggacggg 660  
 gccgaggccg tcctcggccct gggcgagggg gtgttggccc tggccctcga gggcggaaagc 720  
 ggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gagggtcatc 780  
 ccccaggagt tcgcctcaa ggtccaggtg gagggggagg ccctcaggga ggcggtgccc 840  
 cgggtgagcg tcctctccga ccggcagaac caccgggtgg acctccttt ggaggaaggc 900

cgatcctcc tctccgccga gggggactac ggcaaggggc aggagggagt gcccggccag 960  
gtggaggggc cggacatggc cgtggcctac aacgccccct acctcctcga ggcctcgcc 1020  
cccggtgggg accggggcca cctgggcattc tccgggcca cgagcccgag cctcatctgg 1080  
gggacgggg aggggtaccg ggcggtggtg gtgcctca gggtag 1128

<210> 107  
<211> 376  
<212> PRT  
<213> Thermus thermophilus

<400> 107  
Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu  
1 5 10 15  
  
Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr  
20 25 30  
  
Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn  
35 40 45  
  
Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu  
50 55 60  
  
Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser  
65 70 75 80  
  
Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln  
85 90 95  
  
Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser  
100 105 110  
  
Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu  
115 120 125  
  
Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu  
130 135 140  
  
Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr  
145 150 155 160  
  
Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe  
165 170 175  
  
Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro  
180 185 190

Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val
195						200					205				
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val
210					215					220					
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Gly	Ser
225						230			235				240		
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr
245							250					255			
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly
260							265				270				
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg
275						280				285					
Gln	Asn	His	Arg	Val	Asp	Leu	Leu	Leu	Glu	Glu	Gly	Arg	Ile	Leu	Leu
290						295				300					
Ser	Ala	Glu	Gly	Asp	Tyr	Gly	Lys	Gly	Gln	Glu	Glu	Val	Pro	Ala	Gln
305						310			315				320		
Val	Glu	Gly	Pro	Asp	Met	Ala	Val	Ala	Tyr	Asn	Ala	Arg	Tyr	Leu	Leu
					325				330				335		
Glu	Ala	Leu	Ala	Pro	Val	Gly	Asp	Arg	Ala	His	Leu	Gly	Ile	Ser	Gly
						340		345				350			
Pro	Thr	Ser	Pro	Ser	Leu	Ile	Trp	Gly	Asp	Gly	Glu	Gly	Tyr	Arg	Ala
						355		360				365			
Val	Val	Val	Pro	Leu	Arg	Val	Glx								
						370		375							

<210> 108  
<211> 376  
<212> PRT  
<213> Thermus thermophilus

<400> 108															
Met	Asn	Ile	Thr	Val	Pro	Lys	Lys	Leu	Ser	Asp	Gln	Leu	Ser	Leu	
1				5				10				15			
Leu	Glu	Arg	Ile	Val	Pro	Ser	Arg	Ser	Ala	Asn	Pro	Leu	Tyr	Thr	Tyr
					20			25				30			

Leu	Gly	Leu	Tyr	Ala	Glu	Glu	Gly	Ala	Leu	Ile	Leu	Phe	Gly	Thr	Asn
35														45	
Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu
50														60	
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser
65														80	
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln
85														95	
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser
100														110	
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu
115														125	
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu
130														140	
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr
145														160	
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe
165														175	
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro
180														190	
Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val
195														205	
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val
210														220	
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Ser	
225														240	
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr
245														255	
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly
260														270	
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg
275														285	

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu  
290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln  
305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu  
325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly  
340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala  
355 360 365

Val Val Val Pro Leu Arg Val Glx  
370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln  
1 5 10 15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn  
20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp  
35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu  
50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg  
65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg  
85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro  
100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115	120	125
Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe		
130	135	140
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe		
145	150	155
Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg		
165	170	175
Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser		
180	185	190
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp		
195	200	205
Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg		
210	215	220
Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg		
225	230	235
Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu		
245	250	255
Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile		
260	265	270
Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn		
275	280	285
Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu		
290	295	300
Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn		
305	310	315
Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val		
325	330	335
Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala		
340	345	350
Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx		
355	360	365

<210> 110  
<211> 367  
<212> PRT  
<213> Proteus mirabilis

<400> 110  
Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln  
1 5 10 15  
  
Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn  
20 25 30  
  
Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp  
35 40 45  
  
Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu  
50 55 60  
  
Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg  
65 70 75 80  
  
Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg  
85 90 95  
  
Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro  
100 105 110  
  
Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe  
115 120 125  
  
Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe  
130 135 140  
  
Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe  
145 150 155 160  
  
Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg  
165 170 175  
  
Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser  
180 185 190  
  
Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp  
195 200 205  
  
Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu  
210 215 220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly  
225 230 235 240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr  
245 250 255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala  
260 265 270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn  
275 280 285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu  
290 295 300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe  
305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu  
325 330 335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn  
340 345 350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu  
355 360 365

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln  
1 5 10 15

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn  
20 25 30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp  
35 40 45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Glu  
50 55 60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg  
65 70 75 80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg  
85 90 95

Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro  
100 105 110

Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe  
115 120 125

Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe  
130 135 140

Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe  
145 150 155 160

Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg  
165 170 175

Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser  
180 185 190

Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu  
195 200 205

Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg  
210 215 220

Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg  
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val  
245 250 255

Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile  
260 265 270

Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn  
275 280 285

Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu  
290 295 300

Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn  
305 310 315 320

Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val  
325 330 335

Arg	Met	Cys	Leu	Thr	Asp	Ala	Phe	Ser	Ser	Cys	Leu	Ile	Glu	Asn	Cys
340							345							350	
Glu	Asp	Ser	Ser	Cys	Glu	Tyr	Val	Ile	Met	Pro	Met	Arg	Leu		
														365	
355					360										
<210>	112														
<211>	367														
<212>	PRT														
<213>	Pseudomonas	putida													
<400>	112														
Met	His	Phe	Thr	Ile	Gln	Arg	Glu	Ala	Leu	Leu	Lys	Pro	Leu	Gln	Leu
									1	5	10			15	
Val	Ala	Gly	Val	Val	Glu	Arg	Arg	Gln	Thr	Leu	Pro	Val	Leu	Ser	Asn
									20	25				30	
Val	Leu	Leu	Val	Val	Gln	Gly	Gln	Leu	Ser	Leu	Thr	Gly	Thr	Asp	
									35	40				45	
Leu	Glu	Val	Glu	Leu	Val	Gly	Arg	Val	Gln	Leu	Glu	Glu	Pro	Ala	Glu
									50	55				60	
Pro	Gly	Glu	Ile	Thr	Val	Pro	Ala	Arg	Lys	Leu	Met	Asp	Ile	Cys	Lys
									65	70				75	80
Ser	Leu	Pro	Asn	Asp	Ala	Leu	Ile	Asp	Ile	Lys	Val	Asp	Glu	Gln	Lys
									85	90				95	
Leu	Leu	Val	Lys	Ala	Gly	Arg	Ser	Arg	Phe	Thr	Leu	Ser	Thr	Leu	Pro
									100	105				110	
Ala	Asn	Asp	Phe	Pro	Thr	Val	Glu	Glu	Gly	Pro	Gly	Ser	Leu	Thr	Cys
									115	120				125	
Asn	Leu	Glu	Gln	Ser	Lys	Leu	Arg	Arg	Leu	Ile	Glu	Arg	Thr	Ser	Phe
									130	135				140	
Ala	Met	Ala	Gln	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Leu
									145	150				155	160
Glu	Val	Ser	Arg	Asn	Thr	Leu	Arg	Ala	Val	Ser	Thr	Asp	Gly	His	Arg
									165	170				175	
Leu	Ala	Leu	Cys	Ser	Met	Ser	Ala	Pro	Ile	Glu	Gln	Glu	Asp	Arg	His

180	185	190
Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu		
195	200	205
Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile		
210	215	220
Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly		
225	230	235
Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu		
245	250	255
Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala		
260	265	270
Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala		
275	280	285
Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu		
290	295	300
Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe		
305	310	315
Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln		
325	330	335
Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu		
340	345	350
Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu		
355	360	365
<210> 113		
<211> 366		
<212> PRT		
<213> Buchnera aphidicola		
<400> 113		
Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys		
1	5	10
15		
Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn		
20	25	30

Ile	Leu	Ile	Gln	Val	Glu	Asp	Gly	Thr	Leu	Ser	Leu	Thr	Thr	Thr	Asn
35								40							45
Leu	Glu	Ile	Glu	Leu	Ile	Ser	Lys	Ile	Glu	Ile	Ile	Thr	Lys	Tyr	Ile
50								55							60
Pro	Gly	Lys	Thr	Thr	Ile	Ser	Gly	Arg	Lys	Ile	Leu	Asn	Ile	Cys	Arg
65								70							80
Thr	Leu	Ser	Glu	Lys	Ser	Lys	Ile	Lys	Met	Gln	Leu	Lys	Asn	Lys	Lys
									85						90
															95
Met	Tyr	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Tyr	Ile	Leu	Ser	Thr	Leu	Ser
									100						110
Ala	Asp	Thr	Phe	Pro	Asn	His	Gln	Asn	Phe	Asp	Tyr	Ile	Ser	Lys	Phe
									115						120
															125
Asp	Ile	Ser	Ser	Asn	Ile	Leu	Lys	Glu	Met	Ile	Glu	Lys	Thr	Glu	Phe
									130						135
															140
Ser	Met	Gly	Lys	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Leu
									145						150
															155
															160
Glu	Lys	Lys	Asp	Lys	Phe	Leu	Arg	Ser	Val	Ala	Thr	Asp	Gly	Tyr	Arg
									165						170
															175
Leu	Ala	Ile	Ser	Tyr	Thr	Gln	Leu	Lys	Lys	Asp	Ile	Asn	Phe	Phe	Ser
									180						185
															190
Ile	Ile	Ile	Pro	Asn	Lys	Ala	Val	Met	Glu	Leu	Leu	Lys	Leu	Leu	Asn
									195						200
															205
Thr	Gln	Pro	Gln	Leu	Leu	Asn	Ile	Leu	Ile	Gly	Ser	Asn	Ser	Ile	Arg
									210						215
															220
Ile	Tyr	Thr	Lys	Asn	Leu	Ile	Phe	Thr	Thr	Gln	Leu	Ile	Glu	Gly	Glu
									225						230
															235
															240
Tyr	Pro	Asp	Tyr	Lys	Ser	Val	Leu	Phe	Lys	Glu	Lys	Lys	Asn	Pro	Ile
									245						250
															255
Ile	Thr	Asn	Ser	Ile	Leu	Leu	Lys	Ser	Leu	Leu	Arg	Val	Ala	Ile	
									260						265
															270
Leu	Ala	His	Glu	Lys	Phe	Cys	Gly	Ile	Glu	Ile	Lys	Ile	Glu	Asn	Gly
									275						280
															285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp  
290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn  
305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile  
325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu  
340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg  
355 360 365

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtccccct catgcgcgac caggaaggg 39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac 27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116  
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30

<210> 117  
<211> 3514  
<212> DNA  
<213> *Aquifex aeolicus*

<400> 117  
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ataaagatag acgagctcg gaaaaaggca aaggagtatg gatacaaagc tgtcgaaatg 120  
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaaagga 180  
attaagccc taatcgcat ggaagcctac tttaccacgg gttcgaggtt tgacagaag 240  
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatacg 300  
aaggacgaaa agtctaaag aacttaatga agctctcaac cctcgctac aaagaagg 360  
tttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggcctaata 420  
cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaa 480  
aggcggagga atggtaaag aagttcaagg atatattcgg agatgacctt tatttagaac 540  
ttcaagcgaa caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600  
aaaagtacga tgtgaaactc atagcgacgc aggacgccc ctacctcaat cccgaagaca 660  
ggtacgccc cacggttctt atggacttc aaatgaaaaa gaccattcac gaactgagtt 720  
cggaaactt caagtgttca aacgaagacc ttcaacttgc tccacccgag tacatgtgga 780  
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taagacagag gatagaaagg ggacaagcta aggataacta agagtactgg gagaggctcg 1020  
agtacgaact ggaagttata aacaaaatgg gctttgcggg atacttctt atagttcagg 1080  
acttcataaa ctggctaaag aaaaacgaca tacctgttgg acccggagg ggaagtgtcg 1140  
gaggtccct cgtcgcatac gccatcgaa taacggacgt tgaccctata aagcacggat 1200  
tccttttga gaggttctt aaccccgaaa gggttccat gccggatata gacgtggatt 1260  
tctgtcagga caacaggaa aaggtcatag agtacgtaa gaacaagtac ggacacgaca 1320  
acgtagctca gataatcacc tacaacgtaa tgaaggcgaa gcaaacactg agagacgtcg 1380  
caaggccat gggactcccc tactccaccc cgacaaact cgcaaaactc attcctcagg 1440  
gggacgttca gggAACGTTGG ctcaacttgg aagagatgtt caaaacgcgt gtggaggaac 1500  
tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaag aagttcagac 1560  
agatatgcga agaaagtccg gagataaaac agtcgttga gacggccctg aagcttgaag 1620  
gtctcacgg acacacccctt ctccaccccg cgggagttgtt tatagcacca aagcccttga 1680  
gcaacgtcg tcccccttac tacgataaaag agggcgaagt cgcaaccccg tacgacatgg 1740  
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aactgaaact catgaaagaa ctcataaagg aaagacacgg agtggatata aacttcctt 1860  
aacttccct tgacgaccccg aaagtttaca aactccttca ggaaggaaaa accacgggag 1920  
tgttccagct cggaaacggg ggaatgaaag aactccttca gaaactaaag cccgacagct 1980  
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ttgaaacccgt ctttaaggaa acctacggag taatcggttca ttaggaacag gtatgaaaga 2160  
tgtctcagat aacttccggc tttactcccg gagaggcgga taccctcaga aaggcgatag 2220  
gtaagaagaa agcggattta atggctcaga tggaaagacaa gttcatacag ggagcgggtgg 2280

aaaggggata ccctgaagaa aagataagga agctctggga agacatagag aagttcgctt 2340  
cctactcctt caacaagtct cactcggtag cttacggta catctcctac tggaccgcct 2400  
acgttaaagc ccactatccc gcggagttct tcgcgtaaa actcacaact gaaaagaacg 2460  
acaacaagtt cctcaacctc ataaaagacg ctaaactctt cgatttgag atacttcccc 2520  
ccgacataaa caagagtat gttaggattt cgatagaagg tgaaaacagg ataaggttcg 2580  
ggcttgcgag gataaaggga gtgggagagg aaactgctaa gataatcggt gaagctagaa 2640  
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taaacaagaa agtcgtggaa gcactcgtaa aggcaaggc ttttgactt actaagaaaa 2760  
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aggaagttct cggttttac atttcaggc acccccttga caactacgaa aagctcctca 2940  
agaaccgcta cacaccatt gaagatttag aagagtggga caaggaaagc gaagcggcgc 3000  
ttacaggagt tattcaggaa ctcaaagtaa aaaagacgaa aaacggagat tacatggcgg 3060  
tcttcaacct cgttgcacaag acgggactaa tagagtgtgt cgtcttcccggagtttacg 3120  
aagaggcaaa ggaactgata gaagaggaca gagtagtggt agtcaaaggt tttctggacg 3180  
aggaccttga aacggaaaat gtcaagttcg tggtaaaga ggtttctcc cctgaggagt 3240  
tcgcaaagga gatgaggaat acccttata tattcttaaa aagagagcaa gccctaaacg 3300  
gcgttgcga aaaactaaag ggaattattt aaaaacaacag gacggaggac ggatacaact 3360  
tggttctcac ggttgatctg ggagactact tcgttgattt agcactccca caagatatga 3420  
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tttagtaaat aacccttact tccgagtagt cccc 3514

<210> 118  
<211> 1161  
<212> PRT  
<213> Aquifex aeolicus

<400> 118  
Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu  
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Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu  
20 25 30

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly  
35 40 45

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile  
50 55 60

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys  
65 70 75 80

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu  
85 90 95

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

100	105	110
Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp		
115	120	125
Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala		
130	135	140
Cys Leu Lys Gly Val Pro Thr Tyr Tyr Ala Ser Ile Asn Glu Val Lys		
145	150	155
Lys Ala Glu Glu Trp Val Lys Lys Phe Lys Asp Ile Phe Gly Asp Asp		
165	170	175
Leu Tyr Leu Glu Leu Gln Ala Asn Asn Ile Pro Glu Gln Glu Val Ala		
180	185	190
Asn Arg Asn Leu Ile Glu Ile Ala Lys Lys Tyr Asp Val Lys Leu Ile		
195	200	205
Ala Thr Gln Asp Ala His Tyr Leu Asn Pro Glu Asp Arg Tyr Ala His		
210	215	220
Thr Val Leu Met Ala Leu Gln Met Lys Lys Thr Ile His Glu Leu Ser		
225	230	235
240		
Ser Gly Asn Phe Lys Cys Ser Asn Glu Asp Leu His Phe Ala Pro Pro		
245	250	255
Glu Tyr Met Trp Lys Lys Phe Glu Gly Lys Phe Glu Gly Trp Glu Lys		
260	265	270
Ala Leu Leu Asn Thr Leu Glu Val Met Glu Lys Thr Ala Asp Ser Phe		
275	280	285
Glu Ile Phe Glu Asn Ser Thr Tyr Leu Leu Pro Lys Tyr Asp Val Pro		
290	295	300
Pro Asp Lys Thr Leu Glu Glu Tyr Leu Arg Glu Leu Ala Tyr Lys Gly		
305	310	315
320		
Leu Arg Gln Arg Ile Glu Arg Gly Gln Ala Lys Asp Thr Lys Glu Tyr		
325	330	335
Trp Glu Arg Leu Glu Tyr Glu Leu Glu Val Ile Asn Lys Met Gly Phe		
340	345	350
Ala Gly Tyr Phe Leu Ile Val Gln Asp Phe Ile Asn Trp Ala Lys Lys		

355	360	365
Asn Asp Ile Pro Val Gly Pro Gly Arg Gly Ser Ala Gly Gly Ser Leu		
370	375	380
Val Ala Tyr Ala Ile Gly Ile Thr Asp Val Asp Pro Ile Lys His Gly		
385	390	395
Phe Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp		
405	410	415
Ile Asp Val Asp Phe Cys Gln Asp Asn Arg Glu Lys Val Ile Glu Tyr		
420	425	430
Val Arg Asn Lys Tyr Gly His Asp Asn Val Ala Gln Ile Ile Thr Tyr		
435	440	445
Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met		
450	455	460
Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln		
465	470	475
Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr		
485	490	495
Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile		
500	505	510
Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu		
515	520	525
Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg		
530	535	540
His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu		
545	550	555
Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr		
565	570	575
Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp		
580	585	590
Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu		
595	600	605
Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu		

610	615	620
Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly		
625	630	640
Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu		
645	650	655
Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg		
660	665	670
Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys		
675	680	685
His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val		
690	695	700
Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys		
705	710	720
Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu		
725	730	735
Arg Lys Ala Ile Gly Lys Lys Ala Asp Leu Met Ala Gln Met Lys		
740	745	750
Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys		
755	760	765
Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe		
770	775	780
Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala		
785	790	800
Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr		
805	810	815
Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys		
820	825	830
Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val		
835	840	845
Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg		
850	855	860
Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg		

865	870	875	880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr			
885		890	895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala			
900		905	910
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys			
915	920		925
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe			
930	935		940
Gly Ala Pro Lys Glu Glu Val Glu Leu Asp Pro Leu Lys Leu Glu			
945	950		955
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr			
965		970	975
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu			
980		985	990
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu			
995	1000		1005
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu			
1010	1015		1020
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr			
1025	1030		1035
1040			
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Lys			
1045		1050	1055
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val			
1060		1065	1070
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr			
1075	1080		1085
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu			
1090	1095		1100
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn			
1105	1110		1115
1120			
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu			

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile  
1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile  
1155 1160

<210> 119  
<211> 2408  
<212> DNA  
<213> Aquifex aeolicus

<400> 119  
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tacctcttg ccggaccgag gggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180  
gcttgaact gtaaaaatcc ctccaaaggt gagccctgcg gtgagtgcga aaactgcagg 240  
gagatagaca ggggtgtgtt ccctgactta attgaaatgg atgcccctc aaacaggggt 300  
atagacgacg taagggcatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360  
aaggtttaca taatagacga agctcacatg ctcacgaaag aagcttcaa cgctcttta 420  
aaaaccctcg aagagcccccc tcccagaact gtttcgtcc tttgtaccac ggagtacgac 480  
aaaattcttc ccacgatact ctcaaggtgt cagaggataa tcttctcaaa ggtaagaaag 540  
gaaaaagtaa tagagtatct aaaaaagata tgtgaaaagg aagggtatga gtgcgaagag 600  
ggagcccttg aggttctggc tcatgcctct gaagggtgca tgagggatgc agcctctctc 660  
ctggaccagg cgagcggtta cggggaaaggc agggtaacaa aagaagttagt ggagaacttc 720  
ctcggattc tcagtcagga aagcgttagg agtttctga aattgcttct gaactcagaa 780  
gtggacgaag ctataaagtt cctcagagaa ctctcagaaaa agggctacaa cctgaccaag 840  
ttttgggaga tgttagaaga ggaagtgaga aacgcaattt tagtaaagag cctgaaaaat 900  
cccgaaagcg tggttcagaa ctggcaggat tacgaagact tcaaagacta ccctctggaa 960  
gccctcctct acgttgagaa cctgataaac agggtaaag ttgaagcgag aacgagagaa 1020  
cccttaagag cctttgaact cgcggtaata aagagcctta tagtcaaaga cataattccc 1080  
gtatcccagc tcggaagtgt ggttaaggaa accaaaaagg aagaaaagaa agttgaagta 1140  
aaagaagagc caaaagtaaa agaagaaaaa ccaaaggagc aggaagagga cagttccag 1200  
aaagtttaa acgctgtgga cggcaaaatc cttaaaagaa tacttgaagg ggcaaaaagg 1260  
gaagaaagag acggaaaaat cgtcctaag atagaagcct cttatctgag aaccatgaaa 1320  
aaggaatttg actcactaaa ggagacttt ccttttttag agtttgaacc cgtggaggat 1380  
aaaaaaaaac ctcagaagtc cagcgggacg aggctgttt aaaggtaaag gagctcttca 1440  
atgaaaaat actcaaagta cgaagtaaaa gctaaggtca taaaggttag aatgcccgtg 1500  
gaagagatac ggctgtttaa cgcactaata gacggcttgc ccaggtacgc actcacgagg 1560  
acgaaggaaa agggaaaggg agaagtttc gttttagcga ctccttataa agtcaaggaa 1620  
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acggatgagg atttaacttt ttaaagtatg ggtgtatctg agcaaaggtt taagctaaaa 1740  
acaaacctga aacccgcagg ggaccagccg aaagccataa aaaaactcct tgaaaaccta 1800  
aggaaaggcg taaaagaaca aacacttctc ggagtcacgg gaagcggaaa gactttact 1860  
ctagcaaacg taatagcga gtacaacaaa ccaactcttg tggtagttca caacaaaatt 1920  
ctcgccgcac agctatacag ggagttaaa gaactattcc ctgaaaacgc tgttagagtac 1980

tttgtctt actacgacta ttaccaacct gaagcctaca ttcccgaaaa agatttatac 2040  
atagaaaagg acgcgagttt aaacgaaagc tggAACgttt cagacactcc gccacgatat 2100  
ccgttctaga aaggaggac gttatagtag ttgcttcagt ttcttgata tacggactcg 2160  
ggaaacctga gcactacgaa aacctgagga taaaactcca aaggggaata agactgaact 2220  
ttagtaagct cctgagaaaa ctcgttgagc taggatatca gagaaatgac tttgccataa 2280  
agagggctac cttctcggtt aggggagacg tggttgagat agtcccttct cacacggaag 2340  
attacctcgta gaggtagag ttctggacg acgaagttga aagaatagtc ctcatggacg 2400  
ctctgaac 2408

<210> 120  
<211> 473  
<212> PRT  
<213> Aquifex aeolicus

<400> 120  
Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg  
1 5 10 15  
  
Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile  
20 25 30  
  
Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly  
35 40 45  
  
Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys  
50 55 60  
  
Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg  
65 70 75 80  
  
Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala  
85 90 95  
  
Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn  
100 105 110  
  
Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala  
115 120 125  
  
His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140  
  
Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp  
145 150 155 160  
  
Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser  
165 170 175

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu  
                  180                         185                         190  
  
 Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His  
                  195                         200                         205  
  
 Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala  
                  210                         215                         220  
  
 Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe  
                  225                         230                         235                         240  
  
 Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu  
                  245                         250                         255  
  
 Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser  
                  260                         265                         270  
  
 Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu  
                  275                         280                         285  
  
 Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val  
                  290                         295                         300  
  
 Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu  
                  305                         310                         315                         320  
  
 Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala  
                  325                         330                         335  
  
 Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser  
                  340                         345                         350  
  
 Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val  
                  355                         360                         365  
  
 Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro  
                  370                         375                         380  
  
 Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln  
                  385                         390                         395                         400  
  
 Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu  
                  405                         410                         415  
  
 Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu  
                  420                         425                         430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu  
435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro  
450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe  
465 470

<210> 121

<211> 1090

<212> DNA

<213> Aquifex aeolicus

<400> 121

atgcgcgtta aggtggacag ggaggagctt gaagaggttc ttaaaaaaagc aagagaaaagc 60  
acggaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120  
aacttaatcg taagggcaac ggacttgaa aactacctt tagtctccgt aaagggggag 180  
gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatat agtcaagaac 240  
ttaaattccg cttacgtta ctttcatacg gaaggtgaaa aactcgtcat aacgggagga 300  
aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360  
gtagaaggag gagaaacact ttcggaaac cttctcgta acggaataga aaaggttagag 420  
tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480  
gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540  
taaacattga aaagagtgaa gacgagtctt ttgcttactt ctccactccc gagtgaaac 600  
tcgcccgttag ctccctgaaag gagaattccc ggactacatg agtgcatacc ctgaggagtt 660  
ttcggcggaa gtcttggaa agacagagga agtcttaaag gttttaaaga ggttgaaggc 720  
tttaagcgaa ggaaaagttt ttcccgtgaa gattacctt agcgaaaacc ttgcctatctt 780  
tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840  
agagccctt gagataggat tcaacggaaa taccttatgg aggcgcgttga cgccctacgac 900  
agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960  
gattacgaaa aggaaccta caagtgcata ataatgccga tgagggtgta gccatgaaaa 1020  
aagctttaat cttttattt agcttgagcc tttaattcc tgcgttagc gaagccaaac 1080  
ccaagtcttc 1090

<210> 122

<211> 363

<212> PRT

<213> Aquifex aeolicus

<400> 122

Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys  
1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

20	25	30
Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp		
35	40	45
Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu		
50	55	60
Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn		
65	70	75
Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val		
85	90	95
Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu		
100	105	110
Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser		
115	120	125
Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala		
130	135	140
Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr		
145	150	155
160		
Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu		
165	170	175
Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys		
180	185	190
Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn		
195	200	205
Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu		
210	215	220
Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met		
225	230	235
240		
Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu		
245	250	255
Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys		
260	265	270
Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu		

275

280

285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu  
290 295 300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met  
305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr  
325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu  
340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val  
355 360

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

gtggaaacca caatattcca gttccagaaa actttttca caaaaacctcc gaaggagagg 60  
gtcttcgtcc ttcataggaga agagcagtat ctcataagaa ccttttgtc taagctgaag 120  
gaaaagtacg gggagaatta cacgggtctg tggggggatg agataagcga ggaggaattc 180  
tacactgccc ttccgagac cagttatattc ggccgttcaa aggaaaaagc ggtggtcatt 240  
tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300  
ataaaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360  
cagaaacagg aactttcttc ggaacctctg aaatccgtag cgtcttcgg cggtagatgt 420  
gtacaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480  
aaaggataa acgtagaaaa cgatgccctt gaataccctc tccagctcac gggttacaac 540  
ttgatggagc tcaaacttga ggtgaaaaaa ctgatagatt acgcaagtga aaagaaaatt 600  
ttaacactcg atgaggtaaa gagagtagcc ttctcagtct cagaaaaacgt aaacgtattt 660  
gagttcggtt atttactcct cttaaaagat tacggaaaagg ctcttaaagt tttggactcc 720  
ctcatttcct tcggaataca cccccctccag attatggaaa tcctgtcctc ctatgctcta 780  
aaactttaca ccctcaagag gcttgaagag aaggagagg acctgaataa ggcgatggaa 840  
agcgtggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900  
tctaaagagg acttgaagaa cctaatcctc tccctccaga ggatagacgc tttttctaaa 960  
ctttacttcc aggacacagt gcagttgctg gggatttctt gacctcaaga ctggagaggg 1020  
aagtgtgaa aaatacttct catggtgat aatcttttt atgaagtttgcgt 1080  
tttcccggt tct 1093

<210> 124

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro  
1 5 10 15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Gln Tyr Leu Ile  
20 25 30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr  
35 40 45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu  
50 55 60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile  
65 70 75 80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Glu  
85 90 95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val  
100 105 110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu  
115 120 125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg  
130 135 140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu  
145 150 155 160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu  
165 170 175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile  
180 185 190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg  
195 200 205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp  
210 215 220

Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser  
225 230 235 240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser  
245 250 255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly  
260 265 270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe  
275 280 285

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp  
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys  
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser  
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly  
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

atggaaaaag ttttttgga aaaactccag aaaaccttgc acatacccg aggactcctt 60  
tttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggatt 120  
ttatgttaagg aaaacgtacc tggggatgctc gaagttgtcc ctccgtcaaa cacgtaaacg 180  
agctggagga agccttcattt aaaggagaaa tagaagactt taaagtttat aagacaagga 240  
cgtaaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300  
gagcggacat tacataaaga tagaacat aagggaaagt aagaactttg cctatgtcaa 360  
gccccacta agcaggagaa aagtaattat aatagacgac gcccacgcga tgacctctca 420  
ggcggcaaac gctctttaa aggtattgga agagccacct gcggacaccca cctttatctt 480  
gaccacgaac aggcttctg caatcctgcc gactatcctc tccagaacct ttcaagtgg 540  
gttcaaggc ttttcaagtaa aagaggattt ggaatagcg aaagtagacg agggaaatagc 600  
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660  
aaacaaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720  
attcgaaaaag tgggaaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattgg 780  
atctcaaaaa ttgaccgaag agaaaaaaaaga caattacacc taccttctt atacgatcag 840  
actctttaaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900  
cggtcaggcg gattaataaa cggttatgta ttccgttaaca tttaaacctt aatctaaatt 960  
atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020  
ggaagatagg aaccgtgagc ggtgtaaaag t 1051

<210> 126  
<211> 305  
<212> PRT  
<213> Aquifex aeolicus

<400> 126  
Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro  
1 5 10 15  
  
Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr  
20 25 30  
  
Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp  
35 40 45  
  
Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu  
50 55 60  
  
Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys  
65 70 75 80  
  
Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe  
85 90 95  
  
Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg  
100 105 110  
  
Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys  
115 120 125  
  
Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn  
130 135 140  
  
Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile  
145 150 155 160  
  
Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg  
165 170 175  
  
Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu  
180 185 190  
  
Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu  
195 200 205  
  
Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val  
210 215 220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser  
225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile  
245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn  
260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala  
275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala  
290 295 300

Asp  
305

<210> 127  
<211> 630  
<212> DNA  
<213> Aquifex aeolicus

<400> 127  
atgaacttcc tgaaaaagtt cctttactg agaaaagctc aaaagtctcc ttacttcgaa 60  
gagttctacg aagaaaatcga tttgaaccag aaggtaaaag atgcaaggtt tgttagtttt 120  
gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tccttcaat aggtgcggtt 180  
gaggttaaaa acctgaaat agacctctt aaatctttt acgagatact caaaagtgac 240  
gagataaaagg cggcggagat acatggaata accagggaaag acgttgaaaa gtacggaaag 300  
gaaccaaagg aagtaatata cgacttctg aagtacataa aggaaagcgt tctcggtggc 360  
tactacgtga agttgacgt ctcactcggt gagaagtact ccataaaagta cttccagttat 420  
ccaatcatca actacaagtt agacctgtt agttcgtga agagagagta ccagagtggc 480  
aggagtcttg acgaccttat gaagggactc ggttgaaaa taaggcaag gcacaacgcc 540  
cttgaagatg cctacataaac cgctcttctt ttccctaaagt acgtttaccc gaacaggag 600  
tacagactaa aggatctccc gattttcctt 630

<210> 128  
<211> 210  
<212> PRT  
<213> Aquifex aeolicus

<400> 128  
Met Asn Phe Leu Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser  
1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

20

25

30

Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp  
 35 40 45

Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn  
 50 55 60

Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp  
 65 70 75 80

Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu  
 85 90 95

Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr  
 100 105 110

Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser  
 115 120 125

Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn  
 130 135 140

Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly  
 145 150 155 160

Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala  
 165 170 175

Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu  
 180 185 190

Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile  
 195 200 205

Phe Leu  
 210

<210> 129  
<211> 526  
<212> DNA  
<213> Aquifex aeolicus

<400> 129  
atgctcaata aggttttat aataggaaga cttacgggtg accccgttat aacttatcta 60  
ccgagcggaa cgcccgtagt agagttact ctggctaca acagaaggta taaaaaccag 120  
aacggtaat ttcaggagga aagtcaactc tttgacgtaa aggcgtaacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgta tcgttagaggg aagactctcc 240  
caggaaaaagt gggagaaaaga agaaaagaag ttctcaaagg tcaggataat agcggaaaac 300  
gtaagattaa taaacaggcc gaaagggtgc gaacttcaag cagaagaaga ggaggaagtt 360  
cctcccattg aggagggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420  
gaagaggacg aaataccctt ttaatttga ggaggttaaa gtatggtagt gagagctcct 480  
aagaagaaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

<210> 130  
<211> 147  
<212> PRT  
<213> Aquifex aeolicus

<400> 130  
Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val  
1 5 10 15  
  
Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala  
20 25 30  
  
Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser  
35 40 45  
  
His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala  
50 55 60  
  
Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser  
65 70 75 80  
  
Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile  
85 90 95  
  
Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu  
100 105 110  
  
Gln Ala Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu  
115 120 125  
  
Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu  
130 135 140  
  
Ile Pro Phe  
145

<210> 131  
<211> 1472  
<212> DNA

<213> Aquifex aeolicus

<400> 131  
atgcaatttg tggataaact tccctgtgac gaatccgccc agagggcggt tcttggcagt 60  
atgcttgaag acccccggaaa catacctctg gtacttgaat accttaaaga agaagacttc 120  
tgcatacgacg agcacaagct acttttcagg gttcttacaa acctctggc cgagttacggc 180  
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240  
atacctatag actggctcga agaactctac gaggaggcgg tatccccctga cacgcttgag 300  
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcggtata 360  
gaactcattc acaaaggaaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420  
agcaggatattttccatagc gggaaagtgc acatctacgc agttttacca tgtgaaagac 480  
gttgcggaaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540  
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600  
ttaataatac tcgcccgaag acccggtatg gggaaaaccc cctttatgct ctccataatc 660  
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttggaaatgagcaag 720  
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccacttt caagataagg 780  
tcttggaaatgtatcgaatgaa agatttaaag aagtttgcag caagcgcaat agaactcgca 840  
aagtacgaca tatacctcga cgacacacccc gctctacta caacggattt aaggataagg 900  
gcaagaaaagc tcagaaagga aaaggaagtt gagttcgtgg cggtgacta cttgcaactt 960  
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020  
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgc gctctccgt 1080  
gaggtggaaa agaggagtga taaaagaccc cagttcgtgg acctcagaga atccggacag 1140  
atagaacagg acgcagacact aatcctttc ctccacagac ccgagttacta caagaaaaag 1200  
ccaaatccc aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260  
acggacattt tgaagctcgc atttattaaag gagttacacta agtttgcacaa cctagaagcc 1320  
cttcctgaac aacctcctcga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380  
gaaggattcg aagatattga cttctgaaaaa ttaaggttt ataattttt cttggctatc 1440  
cgggtagct caatcggcag agcgggtggc tg 1472

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala

1

5

10

15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu

20

25

30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu

35

40

45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp

50

55

60

Phe	Val	Leu	Ile	Lys	Asp	His	Leu	Glu	Lys	Asn	Leu	Leu	Gln	Lys	
65									75					80	
Ile	Pro	Ile	Asp	Trp	Leu	Glu	Glu	Leu	Tyr	Glu	Glu	Ala	Val	Ser	Pro
				85					90					95	
Asp	Thr	Leu	Glu	Glu	Val	Cys	Lys	Ile	Val	Lys	Gln	Arg	Ser	Ala	Gln
					100				105				110		
Arg	Ala	Ile	Ile	Gln	Leu	Gly	Ile	Thr	Ser	Thr	Gln	Phe	Tyr	His	Val
					115				120				125		
Lys	Asp	Val	Ala	Glu	Glu	Val	Ile	Glu	Leu	Ile	Tyr	Lys	Phe	Lys	Ser
					130				135				140		
Ser	Asp	Arg	Leu	Val	Thr	Gly	Leu	Pro	Ser	Gly	Phe	Thr	Glu	Leu	Asp
					145				150				155		160
Leu	Lys	Thr	Thr	Gly	Phe	His	Pro	Gly	Asp	Leu	Ile	Ile	Leu	Ala	Ala
					165				170				175		
Arg	Pro	Gly	Met	Gly	Lys	Thr	Ala	Phe	Met	Leu	Ser	Ile	Ile	Tyr	Asn
					180				185				190		
Leu	Ala	Lys	Asp	Glu	Gly	Lys	Pro	Ser	Ala	Val	Phe	Ser	Leu	Glu	Met
					195				200				205		
Ser	Lys	Glu	Gln	Leu	Val	Met	Arg	Leu	Leu	Ser	Met	Met	Ser	Glu	Val
					210				215				220		
Pro	Leu	Phe	Lys	Ile	Arg	Ser	Gly	Ser	Ile	Ser	Asn	Glu	Asp	Leu	Lys
					225				230				235		240
Lys	Leu	Glu	Ala	Ser	Ala	Ile	Glu	Leu	Ala	Lys	Tyr	Asp	Ile	Tyr	Leu
					245				250				255		
Asp	Asp	Thr	Pro	Ala	Leu	Thr	Thr	Asp	Leu	Arg	Ile	Arg	Ala	Arg	
					260				265				270		
Lys	Leu	Arg	Lys	Glu	Lys	Glu	Val	Glu	Phe	Val	Ala	Val	Asp	Tyr	Leu
					275				280				285		
Gln	Leu	Leu	Arg	Pro	Pro	Val	Arg	Lys	Ser	Ser	Arg	Gln	Glu	Glu	Val
					290				295				300		
Ala	Glu	Val	Ser	Arg	Asn	Leu	Lys	Ala	Leu	Lys	Glu	Leu	His	Ile	
					305				310				315		320

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser  
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu  
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys  
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala  
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys  
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro  
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly  
420 425 430

Phe Glu Asp Ile Asp Phe  
435

<210> 133

<211> 1526

<212> DNA

<213> Aquifex aeolicus

<400> 133

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gatacaccct cttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcggg 180  
gtagggggag acgcgataaa gttcggttcc cttaacgagg acatctcta ttttgaagcc 240  
gcccttgaac tcgcaaaacg ctacggaaag aaatttagacc ttgaaaagat atcaaaagac 300  
gaaaaggtat acgtggctct tgacagggtt tgtgatttct acagggaaag ccttctcaa 360  
aacagagagg caagttagta cgtaaagagt agggaaatag accctaagt akgagggaaag 420  
tttgatcttg ggtacgcacc ttccagtgaa gcactcgtaa aagtcttaaa agagaacgt 480  
cttttagagg cttaccttga aactaaaaac ctcccttctc ctacgaaggg tttttacagg 540  
gatctcttc ttccggctgt cgtgatccc ataaggatc cgagggaaag agttataagg 600  
ttccgggtggaa ggaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660  
agggtattta aaaaggggga gaacttattc ggtctttacg aggcaaaagga gtatataaag 720  
gaagaaggat ttgcgatact tgtggaaagg tactttgacc ttttgagact tttttccgag 780  
ggaataagga acgttgttgc acccctcggt acagccctga cccaaaatca ggcaaacctc 840  
ctttccaaagt tcacaaaaaa ggtctacatc cttaacgacg gagatgatgc gggaaagaaag 900  
gctatgaaaaa gtgccattcc cctactcctc agtgcaggag tggaaagttt tccccgtttac 960  
ctccccgaag gatacgatcc cgacgagttt ataaaggaat tcgggaaaga ggaattaaga 1020

agactgataa acagctcagg ggagctctt gaaacgctca taaaaaccgc aaggaaaaac 1080  
ttagaggaga aaacgcgtga gttcaggtat tatctggct ttatccga tggagtaagg 1140  
cgcttgctc tggcttcgga gttcacacc aagtacaag ttcctatgga aattttatta 1200  
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac ttcctttaa ggaaaaaattc 1260  
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cctgagttaa aggaactcgc agttaacgccc ttAAACGGAG aggagcattt acttccaaaa 1380  
gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440  
ttacaaaaat ctggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500  
acttaataa attttagag ttagga 1526

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp  
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Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg  
20 25 30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser  
35 40 45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp  
50 55 60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala  
65 70 75 80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys  
85 90 95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp  
100 105 110

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val  
115 120 125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly  
130 135 140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp  
145 150 155 160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

165	170	175
Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys		
180	185	190
Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu		
195	200	205
Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys		
210	215	220
Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys		
225	230	235
Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg		
245	250	255
Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala		
260	265	270
Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val		
275	280	285
Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser		
290	295	300
Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr		
305	310	315
Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys		
325	330	335
Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr		
340	345	350
Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe		
355	360	365
Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu		
370	375	380
Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu		
385	390	395
Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe		
405	410	415
Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile		

420 425 430

Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val  
435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu  
450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp  
465 470 475 480

Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val  
485 490 495

Asn Thr

<210> 135

<211> 705

<212> DNA

<213> Aquifex aeolicus

<400> 135

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atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180  
aacagggcac ttttgacat aagggtcttc gtccacaact tcaatccga ggaagggaaa 240  
gggcttacct ttgttaggatc tcctggagtc ggcaaaactc accttgcggc tgcaacatta 300  
aaagcgattt atgagaagaa gggaaatcaga ggataacttct tcgatacaga ggatctaata 360  
ttcaggttaa aacacttaat ggacgaggaa aaggatacaa agttttaaa aactgtctta 420  
aactcaccgg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480  
gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540  
acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600  
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aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136

<211> 235

<212> PRT

<213> Aquifex aeolicus

<400> 136

Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val  
1 5 10 15

Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20

25

30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala  
 35                          40                          45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu  
 50                          55                          60

Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys  
 65                          70                          75                          80

Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala  
 85                          90                          95

Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr  
 100                        105                        110

Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp  
 115                        120                        125

Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val  
 130                        135                        140

Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg  
 145                        150                        155                        160

Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser  
 165                        170                        175

Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Ser Ser  
 180                        185                        190

Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val  
 195                        200                        205

Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp  
 210                        215                        220

Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser  
 225                        230                        235

&lt;210&gt; 137

&lt;211&gt; 4101

&lt;212&gt; DNA

&lt;213&gt; Thermatoga maritima

&lt;400&gt; 137

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cccgatgcag gtgtggttct cgttccgtg gaaaaattct ccgaagagat agaagacctt 120  
gtgcgtttac tggagaagaa gacgcggttt cgagtcatcg tgaacggtgt tcaaaaaagt 180  
aacggggatc taagggaaa gatactttcc cttctcaacg gtaatgtgcc ttacataaaa 240  
gatgttgttt tcgaaggaaa caggctgatt ctgaaagtgc ttggagattt cgccgggac 300  
aggatcgccct ccaaactcag aagcacgaaa aaacagctcg atgaactgct gcctccgga 360  
acagagatca tgctggaggt tgtggagcct ccggaagatc ttttggaaaaa ggaagtacca 420  
caaccagaaa agagagaaga accaaagggt gaagaattga agatcgagga tgaaaaccac 480  
atcttggac agaaaacccag aaagatcgtc ttccccct caaaaatctt tgagtacaac 540  
aaaaagacat cggtgaaggg caagatcttc aaaatagaga agatcgaggg gaaaagaacg 600  
gtccttctga ttacatcgac agacggagaa gattctctga tctgcaaagt cttcaacgac 660  
gttggaaaagg tcgaaggaa agtatcggt ggagacgtga tcgttgccac aggagacctc 720  
cttctcgaaa acggggagcc caccctttac gtgaaggaa tcacaaaact tcccgaagcg 780  
aaaaggatgg acaaactctcc ggttaagagg gtggagctcc acgcccatac caagttcagc 840  
gatcaggacg caataacaga tgtgaacgaa tatgtgaaac gagccaagga atggggctt 900  
cccgcatag ccctcacgga tcatgggaac gttcaggcca taccttactt ctacgacgac 960  
gcpaaagaag ctgaaataaa gcccattttc ggtatcgaa cgtatcttgt gagtgacgtg 1020  
gagcccgta taaggaatct ctccgacgat tcgacgtttg gagatgcccac gttcgtcg 1080  
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gagatctcaa gaaaaagttc ggagatcacc ggaatcactc aagagatgct ggaaaacaag 1260  
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gcacacaacg ccaacttcga ctacagatt ctgaggctgt ggtcaaaaaa agtgcgttgg 1380  
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ctatacaaac tggttctga ttccatatata aagtacttct acgggtgttcc gaggatcctc 1740  
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gacagagaaa gactgaaaga agtgcattc aaactctaca gaatagcgaa aaaattgaac 1980  
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gttccatga tcacggagt gaagagaacg acgggtcagc acccaggggg gctcatgatc 2940  
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 acggaacagt tcacgccttt c 4101

<210> 138

<211> 1367

<212> PRT

<213> Thermatoga maritima

<400> 138

Met	Lys	Lys	Ile	Glu	Asn	Leu	Lys	Trp	Lys	Asn	Val	Ser	Phe	Lys	Ser
1															15

Leu	Glu	Ile	Asp	Pro	Asp	Ala	Gly	Val	Val	Leu	Val	Ser	Val	Glu	Lys
															20
															30

Phe	Ser	Glu	Glu	Ile	Glu	Asp	Leu	Val	Arg	Leu	Leu	Glu	Lys	Thr	
															35
															40
															45

Arg	Phe	Arg	Val	Ile	Val	Asn	Gly	Val	Gln	Lys	Ser	Asn	Gly	Asp	Leu
															50
															55
															60

Arg	Gly	Lys	Ile	Leu	Ser	Leu	Leu	Asn	Gly	Asn	Val	Pro	Tyr	Ile	Lys
															65
															70
															75
															80

Asp	Val	Val	Phe	Glu	Gly	Asn	Arg	Leu	Ile	Leu	Lys	Val	Leu	Gly	Asp
															85
															90
															95

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Gln

100	105	110
Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val		
115	120	125
Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys		
130	135	140
Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His		
145	150	155
Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile		
165	170	175
Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile		
180	185	190
Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp		
195	200	205
Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val		
210	215	220
Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu		
225	230	235
Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys		
245	250	255
Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu		
260	265	270
Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val		
275	280	285
Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala		
290	295	300
Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala		
305	310	315
Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu		
325	330	335
Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr		
340	345	350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu		

355	360	365
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln		
370	375	380
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg		
385	390	395
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met		
405	410	415
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly		
420	425	430
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr		
435	440	445
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu		
450	455	460
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu		
465	470	475
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro		
485	490	495
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val		
500	505	510
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu		
515	520	525
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys		
530	535	540
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn		
545	550	555
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val		
565	570	575
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu		
580	585	590
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu		
595	600	605
Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr		

610                    615                    620  
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu  
625                    630                    635                    640  
  
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala  
645                    650                    655  
  
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu  
660                    665                    670  
  
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly  
675                    680                    685  
  
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu  
690                    695                    700  
  
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala  
705                    710                    715                    720  
  
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu  
725                    730                    735  
  
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn  
740                    745                    750  
  
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile  
755                    760                    765  
  
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu  
770                    775                    780  
  
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala  
785                    790                    795                    800  
  
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser  
805                    810                    815  
  
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr  
820                    825                    830  
  
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr  
835                    840                    845  
  
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro  
850                    855                    860  
  
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His

865                    870                    875                    880  
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro  
885                    890                    895  
  
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg  
900                    905                    910  
  
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr  
915                    920                    925  
  
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr  
930                    935                    940  
  
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu  
945                    950                    955                    960  
  
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly  
965                    970                    975  
  
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro  
980                    985                    990  
  
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His  
995                    1000                    1005  
  
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu  
1010                    1015                    1020  
  
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly  
1025                    1030                    1035                    1040  
  
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile  
1045                    1050                    1055  
  
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser  
1060                    1065                    1070  
  
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg  
1075                    1080                    1085  
  
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg  
1090                    1095                    1100  
  
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg  
1105                    1110                    1115                    1120  
  
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
1345	1350	1355
Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139  
<211> 567  
<212> DNA  
<213> Thermatoga maritima

<400> 139  
gtgctcgcca tgatatggaa cgacaccgtt tttgcgtcg tagacacaga aaccacggga 60  
accatccct ttgccgaga ccggatagtt gaaatagccg ctgttcctgt cttcaagggg 120  
aagatctaca gaaacaaagc gtttcaactct ctcgtaatc ccagaataag aatccctgcg 180  
ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaaagcgc agacatggac 240  
acagtttacg atctttcag ggattacgtg aagggAACGG tgctcgtgt tcacaacgcc 300  
aacttcgacc tcactttctt ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360  
aattccata tcgacacact cgatcttca gaagagatct ttggaaaggcc tcattctctc 420  
aaatggctct ccgaaagact tggaaaaaaa accacgatac ggcaccgtgc tcttccagat 480  
gccctggta ccgcaagagt ttttgtaaat ttcttggtga aaacagggtc 540  
aacgaattca tacgtggaaa acgggggg 567

<210> 140  
<211> 189  
<212> PRT  
<213> Thermatoga maritima

<400> 140  
Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr  
1 5 10 15  
  
Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile  
20 25 30  
  
Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe  
35 40 45  
  
His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys  
50 55 60  
  
Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp  
65 70 75 80  
  
Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val  
85 90 95  
  
Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys  
100 105 110  
  
Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp  
115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser  
130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp  
145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly  
165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly  
180 185

<210> 141

<211> 1434

<212> DNA

<213> Thermatoga maritima

<400> 141

gtggaagttc tttacaggaa gtacaggcca aagactttt ctgaggttgt caatcaggat 60  
catgtgaaga aggcaataat cggtgctatt cagaagaaca gcgtggcca cggatacata 120  
ttcgcggtc cgagggAAC ggggaagact actcttgcca gaattctcgc aaaatccctg 180  
aactgtgaga acagaaaAGGG agttgaaccc tgcaattcct gcagagcctg cagagagata 240  
gacgaggaa cttcatgga cgtatagag ctcgacgccc cctccaacag aggaatagac 300  
gagatcagaa gaatcagaga cgccgttggaa tacaggccga tggaaaggta atacaaaagtc 360  
tacataatag acgaagtca catgctcacg aaagaagcct tcaacgcgtc cctcaaaaca 420  
ctcgaagaac ctccttccca cgtcggtttc gtgctggaa cgacaaacct tgagaaggtt 480  
cctcccacga ttatctcgag atgtcaggtt ttcgagttca gaaacattcc cgacgagctc 540  
atcgaaaaga ggctccagga agttgcggag gctgaaggaa tagagataga caggaaagct 600  
ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgcgtcac catgctcgag 660  
caggtgtgga agttctcgga agggaaagata gatctcgaga cggtagacacag ggcgcgtcggg 720  
ttgataccga tacagggtgt tcgcgattac gtgaacgcta tctttctgg tgatgtgaaa 780  
agggtcttca ccgttctcgaa cgacgtctat tacagcggga aggactacga ggtgctcatt 840  
caggaagcag tcgaggatct ggtcgaagac ctggaaaggag agagaggggt ttaccaggtt 900  
tcagcgaacg atatagttca ggtttcgaga caacttctga atcttcttag agagataaaag 960  
ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020  
tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080  
cagaaagaag agaagaaaaga aacgggtgaag gcaaaagaag aaaaacagga agacagcgg 1140  
ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200  
tttgcgttc tcagcctctc agaggtgcag tttgacggag aaaaggtgtat tatttcttt 1260  
gattcatcgaa aagctatgca ttacgagttt atgaagaaaa aactgcctga gctggaaaac 1320  
atttttctaa gaaaactcggtt gaaaaaaagta gaaggtaac ttcgactgtat gggaaaagaa 1380  
gaaacaatcg agaaggttt tcagaagatc ctgagattgt ttgaacagga ggg 1434

<210> 142

<211> 478

<212> PRT

<213> Thermatoga maritima

<400> 142

Met	Glu	Val	Leu	Tyr	Arg	Lys	Tyr	Arg	Pro	Lys	Thr	Phe	Ser	Glu	Val
1				5				10							15
Val	Asn	Gln	Asp	His	Val	Lys	Lys	Ala	Ile	Ile	Gly	Ala	Ile	Gln	Lys
					20				25						30
Asn	Ser	Val	Ala	His	Gly	Tyr	Ile	Phe	Ala	Gly	Pro	Arg	Gly	Thr	Gly
					35			40							45
Lys	Thr	Thr	Leu	Ala	Arg	Ile	Leu	Ala	Lys	Ser	Leu	Asn	Cys	Glu	Asn
					50			55							60
Arg	Lys	Gly	Val	Glu	Pro	Cys	Asn	Ser	Cys	Arg	Ala	Cys	Arg	Glu	Ile
					65			70							80
Asp	Glu	Gly	Thr	Phe	Met	Asp	Val	Ile	Glu	Leu	Asp	Ala	Ala	Ser	Asn
					85			90							95
Arg	Gly	Ile	Asp	Glu	Ile	Arg	Arg	Ile	Arg	Asp	Ala	Val	Gly	Tyr	Arg
					100			105							110
Pro	Met	Glu	Gly	Lys	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	His	Met
					115			120							125
Leu	Thr	Lys	Glu	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	Glu	Pro
					130			135							140
Pro	Ser	His	Val	Val	Phe	Val	Leu	Ala	Thr	Thr	Asn	Leu	Glu	Lys	Val
					145			150							160
Pro	Pro	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Val	Phe	Glu	Phe	Arg	Asn	Ile
					165			170							175
Pro	Asp	Glu	Leu	Ile	Glu	Lys	Arg	Leu	Gln	Glu	Val	Ala	Glu	Ala	Glu
					180			185							190
Gly	Ile	Glu	Ile	Asp	Arg	Glu	Ala	Leu	Ser	Phe	Ile	Ala	Lys	Arg	Ala
					195			200							205
Ser	Gly	Gly	Leu	Arg	Asp	Ala	Leu	Thr	Met	Leu	Glu	Gln	Val	Trp	Lys
					210			215							220
Phe	Ser	Glu	Gly	Lys	Ile	Asp	Leu	Glu	Thr	Val	His	Arg	Ala	Leu	Gly
					225			230							240

Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser  
245 250 255

Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser  
260 265 270

Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val  
275 280 285

Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp  
290 295 300

Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys  
305 310 315 320

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile  
325 330 335

Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu  
340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr  
355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg  
370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile  
385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val  
405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys  
420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys  
435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu  
450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly  
465 470 475

<210> 143  
<211> 1098

<212> DNA

<213> Thermatoga maritima

<400> 143

atgaaagtaa ccgtcacgac tcttgaattt aaagacaaaa taaccatcgc ctcaaaagcg 60  
ctcgaaaga aatccgtgaa acccattttt gctggatttc ttgcgaagt gaaagatgga 120  
aatttctaca tctgcgcacg cgatctcgag accggagtca aagcaaccgt gaatgccgt 180  
gaaatctccg gtgaggcacg ttttggtt ccaggagatg tcattcagaa gatggtaag 240  
gttctccag atgagataac ggaactttct ttagaggggg atgctctgt tataagttct 300  
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttccaga gataacgcct 360  
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggtgaaaag 420  
gtcatcttcg ccgcgtccaa agacgagtcc atgcgaaatc tgaatggagt tttctggaa 480  
ctccacaaga atcttcctcg gctgggtgca agtgatggtt tcagacttgc acttgctgaa 540  
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600  
gttcaaaacg tgctggacaa cacaacggag ccgactataa ccgtgaggtt cgatggaaga 660  
agggttctc tgtcgacaaa tgatgtgaa acggtgatga gagtggtcga cgctgaattt 720  
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtggtggt ttccagaaaa 780  
gaactcaggg aatcttgaa gagggtgatg gtgattgcca gcaagggaaag cgagtccgtg 840  
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagccccga ttatggagaa 900  
gtggtcgtg aagttgaagt tcaaaaagaa gggaaagatc tcgtgatcg ttcaacccg 960  
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020  
gattctacca gtccatgtca gataaatcca ctcgatattt ctggataacct ttacatagtg 1080  
atgcccattca gactggca 1098

<210> 144

<211> 366

<212> PRT

<213> Thermatoga maritima

<400> 144

Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile  
1 5 10 15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly  
20 25 30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp  
35 40 45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly  
50 55 60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys  
65 70 75 80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu  
85 90 95

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala  
100 105 110

Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu  
115 120 125

Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala  
130 135 140

Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu  
145 150 155 160

Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu  
165 170 175

Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Ala Ser Phe Leu  
180 185 190

Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr  
195 200 205

Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu  
210 215 220

Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe  
225 230 235 240

Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val  
245 250 255

Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile  
260 265 270

Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val  
275 280 285

Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu  
290 295 300

Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro  
305 310 315 320

Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu  
325 330 335

Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp  
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala  
355 360 365

<210> 145  
<211> 972  
<212> DNA  
<213> Thermatoga maritima

<400> 145  
atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60  
ctcctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120  
gatttcataa ggtctttact caggacaaag acgatcttt ccaacaagac gatcattgac 180  
atcgtaatt tcgatgagtg gaaagcacag gagcagaagc gtctcggtga actttgaaa 240  
aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacagggtgg aaaggagta 300  
gcgcgtggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtgatc agaaaagcgc 360  
ttcagggaga atggtttgtt catcgataaa gatgcccctc agctgtttt ctccaagggtt 420  
ggaacgaacg acctgtatcat agaaagggag attgaaaaac tgaaagctt ttccgaggac 480  
agaaaagataa cggtagaaga cgtggaaagag gtcgtttta cctatcagac tccgggatac 540  
gatgatTTTt gctttgtgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600  
cagctgtgga aaaccacaga gtcgtgggtt attgccactg tccttgcgaa tcacttctt 660  
gatctcttca aaatcctcgt tcttgtgaca aagaaaagat actacacctg gcctgatgtg 720  
tccaggggtt ccaaagagct gggaaattccc gttcctcggtg tggctcggtt cctcggtttc 780  
tcctttaaga cctggaaattt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840  
gttagaaaga tactgaggga tctctacgt ctggacagag ccgtgaaaag cgaagaagat 900  
ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960  
agagatgaag aa 972

<210> 146  
<211> 324  
<212> PRT  
<213> Thermatoga maritima

<400> 146  
Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu  
1 5 10 15  
  
Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile  
20 25 30  
  
His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg  
35 40 45  
  
Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe  
50 55 60

Asp Glu Trp Lys Ala Gln Glu Gln Lys Arg Leu Val Glu Leu Leu Lys  
65 70 75 80

Asn Val Pro Glu Asp Val His Ile Phe Ile Arg Ser Gln Lys Thr Gly  
85 90 95

Gly Lys Gly Val Ala Leu Glu Leu Pro Lys Pro Trp Glu Thr Asp Lys  
100 105 110

Trp Leu Glu Trp Ile Glu Lys Arg Phe Arg Glu Asn Gly Leu Leu Ile  
115 120 125

Asp Lys Asp Ala Leu Gln Leu Phe Phe Ser Lys Val Gly Thr Asn Asp  
130 135 140

Leu Ile Ile Glu Arg Glu Ile Glu Lys Leu Lys Ala Tyr Ser Glu Asp  
145 150 155 160

Arg Lys Ile Thr Val Glu Asp Val Glu Glu Val Val Phe Thr Tyr Gln  
165 170 175

Thr Pro Gly Tyr Asp Asp Phe Cys Phe Ala Val Ser Glu Gly Lys Arg  
180 185 190

Lys Leu Ala His Ser Leu Leu Ser Gln Leu Trp Lys Thr Thr Glu Ser  
195 200 205

Val Val Ile Ala Thr Val Leu Ala Asn His Phe Leu Asp Leu Phe Lys  
210 215 220

Ile Leu Val Leu Val Thr Lys Lys Arg Tyr Tyr Thr Trp Pro Asp Val  
225 230 235 240

Ser Arg Val Ser Lys Glu Leu Gly Ile Pro Val Pro Arg Val Ala Arg  
245 250 255

Phe Leu Gly Phe Ser Phe Lys Thr Trp Lys Phe Lys Val Met Asn His  
260 265 270

Leu Leu Tyr Tyr Asp Val Lys Lys Val Arg Lys Ile Leu Arg Asp Leu  
275 280 285

Tyr Asp Leu Asp Arg Ala Val Lys Ser Glu Glu Asp Pro Lys Pro Phe  
290 295 300

Phe His Glu Phe Ile Glu Glu Val Ala Leu Asp Val Tyr Ser Leu Gln  
305 310 315 320

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> Thermatoga maritima

<400> 147

atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60  
gaaaagtctg aaggaatatac catcctcata aatggagaag atctctcgta tccgagagaa 120  
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180  
gagatagatc ccgagggggaa gaacataggc atagacgcaca tcagaacgat aaaggacttc 240  
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300  
atgacccagc aggcggcgaa cgcggttctg aaggcccttg aagaaccacc agaatacgct 360  
gtgatcggttc tgaacactcg ccgcgtggcat tatctactgc cgacgataaa gagccgagtg 420  
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480  
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaaggctac 540  
aaacttggtg cgaaaaaaact ttctggattt atggaaagtc tcaaagttt ggagacggaa 600  
aaactcttga aaaaggtcct ttcaaaaggc ctcgaagggtt atctcgcatg tagggagctc 660  
ctggagagat tttcaaaaggt ggaatcgaag gaattcttg cgcttttga tcaggtgact 720  
aacacgataa cagaaaaaga cgcggttctt ttgatccaga gactgacaag aatcattctc 780  
cacgaaaaca catggaaaag cgttgaagat caaaaaagcg tgtcttcct cgattcaatt 840  
ctcagggtga agatagcgaa tctgaacaac aaactcactc tcatgaacat cctcgcgata 900  
cacagagaga gaaagagagg tgtcaacgct tggagc 936

<210> 148

<211> 311

<212> PRT

<213> Thermatoga maritima

<400> 148

Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu  
1 5 10 15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly  
20 25 30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr  
35 40 45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro  
50 55 60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe  
65 70 75 80

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His			
85	90	95	
Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala			
100	105	110	
Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg			
115	120	125	
Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val			
130	135	140	
Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly			
145	150	155	160
Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala			
165	170	175	
Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu			
180	185	190	
Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser			
195	200	205	
Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe			
210	215	220	
Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr			
225	230	235	240
Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr			
245	250	255	
Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser			
260	265	270	
Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn			
275	280	285	
Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys			
290	295	300	
Arg Gly Val Asn Ala Trp Ser			
305	310		

<210> 149

<211> 423  
<212> DNA  
<213> Thermatoga maritima

<400> 149  
atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60  
tacacgctca gcggaaactcc agtcaccacc ttccacccatag cggtgacacgg ggttcccaga 120  
aagaacgcgc cggacgacgc tcaaaccgact gatttcttca ggatcgtcac ctggaaaga 180  
ctggcagagt tcgctagaac ctatctcacc aaaggaaaggc tcgttctcggt cgaagggtgaa 240  
atgagaatga gaagatggaa aacacccact ggagaaaaga gggttatctcc ggaggttgc 300  
gcaaacgttg tttagattcat ggacagaaaaa cctgctgaaa cagtttagcga gactgaagag 360  
gagctggaaa taccggaaaga agactttcc agcgataacct tcagtgaaga tgaaccacca 420  
ttt 423

<210> 150  
<211> 141  
<212> PRT  
<213> Thermatoga maritima

<400> 150  
Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp  
1 5 10 15  
  
Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr  
20 25 30  
  
Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln  
35 40 45  
  
Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe  
50 55 60  
  
Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu  
65 70 75 80  
  
Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser  
85 90 95  
  
Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala  
100 105 110  
  
Glu Thr Val Ser Glu Thr Glu Glu Leu Glu Ile Pro Glu Glu Asp  
115 120 125  
  
Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe  
130 135 140

<210> 151  
 <211> 1353  
 <212> DNA  
 <213> Thermatoga maritima

<400> 151  
 atgcgtgttc ccccgacaa cttagaggcc gaagttgctg tgctcggaa catattgata 60  
 gatccgtcgtaataaacga cgttcttcaa atttgagcc acgaagattt ctatctgaaa 120  
 aaacaccaac acatcttcag agcgatggaa gagcttacg acgaaggaaa accgggtggac 180  
 gtgggttccg tctgtgacaa gcttcaaagc atggaaaac tcgaggaagt aggtggagat 240  
 ctgaaagtggcccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgac 300  
 gagatcgta aggaaaaatc cattctgagg aaactcattt agatctccag aaaaatctca 360  
 gaaagtgcct acatgaaaga agatgtggag atcctgctcg acaacgcaga aaagatgatc 420  
 ttcgagatct cagagatgaa aacgacaaaaa tcctacgatc atctgagagg catcatgcac 480  
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga accgggtgtg 540  
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600  
 agctccgatc tggtataat agcagcgaga ccctccatgg gaaaaacccct cttcgactc 660  
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcgaaatattt cagtcgag 720  
 atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccgggtgt ggatcttac 780  
 agcatcagaa caggatacct ggatcaggag aagtggaaa gactcacaat agccggcttct 840  
 aaactctaca aagcacccat agttgtggac gatgagtcac tcctcgatcc gcgatcggt 900  
 agggcaaaag cgagaaggat gaaaaaaagaa tacatgtaa aagccatgg tggactat 960  
 ctccagctca tgcacccatggaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020  
 tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatagc gcttcacag 1080  
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcaggaa 1140  
 tccggcgcgatagaacagga cgcagacaca gtcatcttca tctacaggg ggaatattac 1200  
 agagcaaaa aatccaaaga gaaagcaag cttcacgaac ctcacgaagc taaaatcata 1260  
 ataggtaaac agagaaacgg tcccgttga acgatcactc tggatcttgc cccagaacg 1320  
 gttacgttcc atgaagtcga tggatgtcat tca 1353

<210> 152  
 <211> 451  
 <212> PRT  
 <213> Thermatoga maritima

<400> 152  
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly  
 1 5 10 15  
  
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu  
 20 25 30  
  
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala  
 35 40 45  
  
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50	55	60	
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp			
65	70	75	80
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala			
85	90	95	
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu			
100	105	110	
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp			
115	120	125	
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser			
130	135	140	
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His			
145	150	155	160
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile			
165	170	175	
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu			
180	185	190	
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala			
195	200	205	
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg			
210	215	220	
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu			
225	230	235	240
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly			
245	250	255	
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp			
260	265	270	
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val			
275	280	285	
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala			
290	295	300	
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr			

305	310	315	320
Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu			
325		330	335
Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp			
340		345	350
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg			
355	360	365	
Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile			
370	375	380	
Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr			
385	390	395	400
Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu			
405	410	415	
Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile			
420	425	430	
Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val			
435	440	445	
Val His Ser			
450			

<210> 153  
 <211> 1695  
 <212> DNA  
 <213> Thermatoga maritima

<400> 153  
 gtgattcctc gagaggtcat cgaggaaata aaagaaaaagg ttgacatcg agaggtcatt 60  
 tccgagtacg tgaatcttac ccgggttaggt tcctcctaca gggctcttg tccctttcat 120  
 tcagaaacca atccttcttt ctacgttcat ccgggtttga agatataccca ttgtttcggc 180  
 tgcgggtgcga gtggagacgt catcaaattt cttcaagaaa tggaaaggat cagtttccag 240  
 gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300  
 gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtacgtc 360  
 aaagagctgg agaaatcgaa agaggcaaaa gactattaa aaagcagagg cttctctgaa 420  
 gaagatatacg caaaggctgg ctttgggtac gtccccaga gatccagcat ctctatagaa 480  
 gttgcagaag gcatgaacat aacactggaa gaacttgtca gatacggtat cgcgctgaaa 540  
 aagggtgatc gattcggtga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600  
 atgggtcata ttgtggcttt tggtggcgt gcttcggca acgaagaacc gaagtatttg 660  
 aactctccag agaccaggtta ttttcgaag aagaagaccc tttttctt cgttgaggcg 720

aaaaaaagtgg caaaagaggt tggtttttc gtcatcaccg aaggctactt cgacgcgctc 780  
gcattcagaa aggatgaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840  
gaggcgattc taaaacttgc ggcgtattcg aaaaacgtca tactgtgtt cgataatgac 900  
aaagcaggct tcagagccac tctcaaattcc ctcgaggatc tcctagacta cgaattcaac 960  
gtgcttgtgg caaccccttc tccttacaaa gaccagatg aactcttca gaaagaagga 1020  
gaagggttcat tgaaaaagat gctgaaaaac tcgcgttgcg tgcataattt tctggtgacg 1080  
gctgggtgagg tcttcttgc caggaacagc cccgcgggtg tgagatccta cctttcttc 1140  
ctcaaagggtt gggtccaaaaa gatgagaagg aaaggatatt taaaacacat agaaaatctc 1200  
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agatttgaa ctttttgaa 1260  
agcgcacaggct ctaacactat gcctgttcat gagaccaagt cgtcaaaggt ttacgatgag 1320  
gggagaggac tggcttattt gttttgaac tacgaggatt tgagggaaaa gattctggaa 1380  
ctggacttag aggtactgga agataaaaac gcgagggagt tttcaagag agtctcaetg 1440  
ggagaagatt tgaacaaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500  
gagacaatag aaagcattcc tcctccaaag gatcccaga aattcctcgg tgacctctcc 1560  
gaaaaggtaa aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaag 1620  
aaagcttcaa acgatgaaga aaggcgttctt cttctctcta taaaagtgaa tctcctcaga 1680  
aaaataaaga ggagg 1695

<210> 154

<211> 565

<212> PRT

<213> Thermatoga maritima

<400> 154

Met	Ile	Pro	Arg	Glu	Val	Ile	Glu	Glu	Ile	Lys	Glu	Lys	Val	Asp	Ile
1					5				10				15		

Val	Glu	Val	Ile	Ser	Glu	Tyr	Val	Asn	Leu	Thr	Arg	Val	Gly	Ser	Ser
									25				30		

Tyr	Arg	Ala	Leu	Cys	Pro	Phe	His	Ser	Glu	Thr	Asn	Pro	Ser	Phe	Tyr
												35		40	

Val	His	Pro	Gly	Leu	Lys	Ile	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Ser
												50		55	

Gly	Asp	Val	Ile	Lys	Phe	Leu	Gln	Glu	Met	Glu	Gly	Ile	Ser	Phe	Gln
									65				75		80

Glu	Ala	Leu	Glu	Arg	Leu	Ala	Lys	Arg	Ala	Gly	Ile	Asp	Leu	Ser	Leu
									85			90		95	

Tyr	Arg	Thr	Glu	Gly	Thr	Ser	Glu	Tyr	Gly	Lys	Tyr	Ile	Arg	Leu	Tyr
												100		105	

Glu	Glu	Thr	Trp	Lys	Arg	Tyr	Val	Lys	Glu	Leu	Glu	Lys	Ser	Lys	Glu
									115			120		125	

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala  
130 135 140

Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu  
145 150 155 160

Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly  
165 170 175

Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg  
180 185 190

Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly  
195 200 205

Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu  
210 215 220

Thr Arg Tyr Phe Ser Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala  
225 230 235 240

Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr  
245 250 255

Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala  
260 265 270

Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala  
275 280 285

Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe  
290 295 300

Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn  
305 310 315 320

Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe  
325 330 335

Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg  
340 345 350

Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg  
355 360 365

Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp  
370 375 380

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu  
 385 390 395 400  
 Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu  
 405 410 415  
 Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr  
 420 425 430  
 Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe  
 435 440 445  
 Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu  
 450 455 460  
 Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu  
 465 470 475 480  
 Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys  
 485 490 495  
 Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro  
 500 505 510  
 Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile  
 515 520 525  
 Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn  
 530 535 540  
 Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg  
 545 550 555 560  
 Lys Ile Lys Arg Arg  
 565

<210> 155  
 <211> 804  
 <212> DNA  
 <213> Thermus thermophilus

<400> 155  
 atggctctac acccggtca ccctggggca ataatcggtc acgaggccgt tctcgccctc 60  
 cttccccgcc tcaccgccc gaccctgctc ttctccggcc ccgaggggtt gggcgccgc 120  
 accgtggccc gctggtaacgc ctgggggctc aaccgcggct tccccccgcc ctccctgggg 180  
 gagcacccgg acgtcctcga ggtggggccc aaggccccggg acctccgggg ccggggccgag 240

gtgcggctgg aggaggtggc gcccctttg gagtggtgct ccagccaccc ccgggagcgg 300  
gtgaagggtgg ccatccttgg a ctcggcccac ctccctcaccg aggccgcccc caacgcctc 360  
ctcaagctcc tggaggagcc cccttcctac gcccgcattcg tcctcatcg cccaaagccgc 420  
gccaccctcc tccccccctt ggccctccgg gccacggagg tggcattcg ccccggtgccc 480  
gaggaggccc tgccgcgcctt cacccaggac ccggagctcc tccgctacgc cgccggggcc 540  
ccggggccgc tccttagggc ctcaggac ccggagggtt accgggccc catggccagg 600  
gcgcaaagggtt tcctgaaaagc cccgccttgg gagcgcctcg ctggcttcg ggagctttt 660  
gccgaggagg aggggggtcca cccgccttccac gccgtcctaa agcgcgggaa gcacccctt 720  
gccctggagc gggcgccgggaa ggccctggag ggtaacgtga gccccgagct ggccctcgcc 780  
cgctggcct tagacttaga gaca 804

<210> 156

<211> 268

<212> PRT

<213> Thermus thermophilus

<400> 156

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala

1

5

10

15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser

20

25

30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp

35

40

45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp

50

55

60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu

65

70

75

80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His

85

90

95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu

100

105

110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro

115

120

125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu

130

135

140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro

145

150

155

160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr  
165 170 175

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu  
180 185 190

Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro  
195 200 205

Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu  
210 215 220

Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu  
225 230 235 240

Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu  
245 250 255

Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr  
260 265

<210> 157

<211> 729

<212> DNA

<213> Thermus thermophilus

<400> 157

atgctggacc tgagggaggt gggggaggcg gagtggaaagg ccctaaagcc cttttggaa 60  
agcgtccccg agggcgccc cgtcctcctc ctggacccta agccaagccc ctccgggcg 120  
gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180  
cggcacctgg aaaaccgggc caagcgctg gggctcaggc tcccggcgg ggtggccag 240  
tacctggcct ccctggaggg ggacctcgag gcccctggc gggagctgga gaagcttgcc 300  
ctcctctccc caccctcac cctggagaag gtggagaagg tggtggccct gaggcccccc 360  
ctcacggct ttgacctggt gcgcctccgtc ctggagaagg accccaagga ggccctcctg 420  
cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480  
tggcagttcg ccctcctcgc ccgggccttc ttccctcctcc gggaaaaccc caggcccaag 540  
gaggaggacc tcgccccct cgaggcccac ccctacgccc cccgccgcg cctggaggcg 600  
gcgaagcgcc tcacggaaga ggccctcaag gaggccctgg acgcctcat ggaggcggaa 660  
aagagggcca agggggggaa agaccctgg ctgcctcgtt aggcggcggt cctccgcctc 720  
ggccgttga 729

<210> 158

<211> 292

<212> PRT

<213> Thermus thermophilus

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu  
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr  
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly  
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala  
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu  
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg  
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His  
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val  
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg  
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys  
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu  
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu  
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala  
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg  
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His  
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu  
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg  
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu  
275 280 285

Arg Leu Ala Arg  
290

<210> 159

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 159

gtgtgtcata tgagtaagga tttcgccac ctgcacc

37

<210> 160

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 160

gtgtgtggat ccggggacta ctcgaaacta aggg

34

<210> 161

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 161

gtgtgtcata tggaaaccac aatattccag ttccag

36

<210> 162

<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 162  
gttgtggat ccttatccac catgagaagt attttcac 39

<210> 163  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 163  
gtgtgtcata tggaaaaagt ttttttggaa aaaaactcca g 41

<210> 164  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 164  
gttgtggat ccttaatccg cctgaacggc taacg 35

<210> 165  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 165  
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g 41

<210> 166

<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 166  
tgtgtggat ccttaaaaca gcctcgccc gctgga 36

<210> 167  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 167  
tgtgtcata tgcgcgttaa ggtggacagg gag 33

<210> 168  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 168  
tgtgtctcga gtcatggcta caccctcatc ggcatt 35

<210> 169  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 169  
tgtgtcata tgctcaataa ggttttata ataggaagac ttacggg 47

<210> 170

<211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 170  
 gtgtggatcc taaaaaaggt atttcgtcct cttcatcg 39

<210> 171  
 <211> 807  
 <212> DNA  
 <213> Thermus thermophilus

<400> 171  
 atggctcgag gcctgaaccg cgtttcctc atcggcgccc tcgccacccg gccggacatg 60  
 cgctacaccc cggcggggct cgccatttt gacctgaccc tcgcggtca ggacctgctt 120  
 cttdccgata acggggggga accggaggtg tccttgtacc accgggttag 90 gctcttaggc 180  
 cggcaggcgg agatgtgggg cgaccttgc gaccaaggc agctcgtctt cgtggaggc 240  
 cgcttgagt accgcccagtg gaaaagggag ggggagaagc ggagcgagct ccagatccgg 300  
 gcccacttcc ggacccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360  
 agcccaggct cccgcggcgc ctgaaccagg tcttcctcat gggcaacctg acccgggacc 420  
 cggaaactccg ctacaccccc cagggcaccc cggtggcccg gctgggcctg gcggtgaacg 480  
 agcgccgcca gggggcggag gagcgcaccc acttcgtgga gttcaggcc tggcgcgacc 540  
 tggcggagtggcccgag ctgaggaagg ggcacggcctt ttcgtgatc ggcagggtgg 600  
 tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccctg gtggaggccc 660  
 tcaggctgga ggcggccacc cgtggacctg cccaggcccg cggAACAGGT 720  
 cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac ttccgcgg 780  
 aggaggattt gccgtttga gcacgaa 807

<210> 172  
 <211> 266  
 <212> PRT  
 <213> Thermus thermophilus

<400> 172  
 Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr  
 1 5 10 15

Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu  
 20 25 30

Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro  
 35 40 45

Glu	Val	Ser	Trp	Tyr	His	Arg	Val	Arg	Leu	Leu	Gly	Arg	Gln	Ala	Glu
50					55						60				
Met	Trp	Gly	Asp	Leu	Leu	Asp	Gln	Gly	Gln	Leu	Val	Phe	Val	Glu	Gly
65				70					75				80		
Arg	Leu	Glu	Tyr	Arg	Gln	Trp	Glu	Arg	Glu	Gly	Glu	Lys	Arg	Ser	Glu
		85						90				95			
Leu	Gln	Ile	Arg	Ala	Asp	Phe	Leu	Asp	Pro	Leu	Asp	Asp	Arg	Gly	Lys
		100					105					110			
Lys	Arg	Ala	Glu	Asp	Ser	Arg	Gly	Gln	Pro	Arg	Leu	Arg	Ala	Ala	Leu
		115				120				125					
Asn	Gln	Val	Phe	Leu	Met	Gly	Asn	Leu	Thr	Arg	Asp	Pro	Glu	Leu	Arg
		130				135				140					
Tyr	Thr	Pro	Gln	Gly	Thr	Ala	Val	Ala	Arg	Leu	Gly	Leu	Ala	Val	Asn
	145				150				155			160			
Glu	Arg	Arg	Gln	Gly	Ala	Glu	Glu	Arg	Thr	His	Phe	Val	Glu	Val	Gln
		165					170					175			
Ala	Trp	Arg	Asp	Leu	Ala	Glu	Trp	Ala	Ala	Glu	Leu	Arg	Lys	Gly	Asp
		180				185					190				
Gly	Leu	Phe	Val	Ile	Gly	Arg	Leu	Val	Asn	Asp	Ser	Trp	Thr	Ser	Ser
		195				200				205					
Ser	Gly	Glu	Arg	Arg	Phe	Gln	Thr	Arg	Val	Glu	Ala	Leu	Arg	Leu	Glu
		210				215				220					
Arg	Pro	Thr	Arg	Gly	Pro	Ala	Gln	Ala	Cys	Pro	Gly	Arg	Arg	Asn	Arg
	225				230				235			240			
Ser	Arg	Glu	Val	Gln	Thr	Gly	Gly	Val	Asp	Ile	Asp	Glu	Gly	Leu	Glu
		245						250			255				
Asp	Phe	Pro	Pro	Glu	Glu	Asp	Leu	Pro	Phe						
		260					265								

<210> 173  
<211> 992  
<212> DNA  
<213> *Bacillus stearothermophilus*

<400> 173  
aattccgaca ttcaattga atcggttatt ccgcggaaa aagaaggcaa gttgctcggtt 60  
gatgtgaaaa gaccggggag catcgactg caggcgcgt tttctctga aatcgtaaa 120  
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca acttttgac gatcatccgc 180  
tcggggact cagaattccg cctcaatggg ctaaacccg acgaatatcc gcgcctccgg 240  
caaatttgaag aagaaaaacgt gtttcaaattc ccggctgatt tattgaaaac cgtgattcgg 300  
caaacgttgt tcgcgttacatcgaa acgcgcggaa tcttgacagg tgtcaactgg 360  
aaagttaaac atggcgagct tgtctgcaca gcgaccgaca gtcatcgctt agccatgcgc 420  
aaagtgaaaa tttagtccgaa aatgaagta tcataacaacg tcgtcatccc tggaaaaaagt 480  
cttaatgagc tcagcaaaat ttggatgac ggcaaccacc cggtggacat cgtcatgaca 540  
gccaatcaag tgctatttaa ggccgagcac ctctcttct tttcccggtt gcttgacggc 600  
aactatccgg agacggcccg ctgttccaa acagaaagca aaacgaccat gatcgtaat 660  
gcaaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720  
aacgttgtga aactgacgac gttccttggaa ggaatgctcg aaatttcttc gatttctccg 780  
agatcggaa agtgacggag cagctgcaaa cggagtctt tgaagggaa gagttgaaca 840  
tttcgttcag cgcgaaatataat atgatggacg cgttgcgggc gcttgcgttgc acagacattt 900  
caaattcagct tcactggggc catgcggccg ttccgttgc gcccgttca accgattcga 960  
tgcttcagct cattttggccg gtgagaacat at 992

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<210> 174
<211> 334
<212> PRT
<213> Bacillus stearothermophilus

<400> 174
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
      1           5           10          15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
      20          25          30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
      35          40          45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
      50          55          60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
      65          70          75          80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
      85          90          95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
      100         105         110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu

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115	120	125
Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys		
130	135	140
Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly		
145	150	155
Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His		
165	170	175
Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu		
180	185	190
His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr		
195	200	205
Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala		
210	215	220
Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu		
225	230	235
Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu		
245	250	255
Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu		
260	265	270
Gln Thr Glu Ser Leu Glu Gly Glu Leu Asn Ile Ser Phe Ser Ala		
275	280	285
Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln		
290	295	300
Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His		
305	310	315
Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr		
325	330	

<210> 175  
<211> 492  
<212> DNA  
<213> *Bacillus stearothermophilus*

<400> 175

atgattaacc gcgtcatttt ggtcgccagg ttaacgagag atccggagtt gcgttacact 60  
ccaagcggag tggctgttgc cacgtttacg ctcgcggtca accgtccgtt tacaaaatcg 120  
cagggcgagc gggaaacgga ttttattcaa tgtgtcggtt ggccgcgc 180  
gtcgc当地 act tttgaaaaa ggggagctt gctgggtcg atggccgact gcaaaccgc 240  
agctatgaaa atcaagaagg tcggcgtgtg tacgtacgg aagtggtggc tgatagcg 300  
caatttcttg agccgaaagg aacgagcagc cagcgggggg cgacagcagg cggtactat 360  
ggggatccat tcccattcgg gcaagatcg aaccaccaat atccgaacga aaaagggtt 420  
ggccgcatcg atgacgatcc ttgc当地 aacggccagc cgatcgatat ttctgatgat 480  
gatttgc当地 tt 492

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu  
1 5 10 15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala  
20 25 30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg  
35 40 45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu  
50 55 60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Tyr Tyr  
65 70 75 80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg  
85 90 95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly  
100 105 110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln  
115 120 125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp  
130 135 140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp  
145 150 155 160

Asp Leu Pro Phe

<210> 177  
<211> 1044  
<212> DNA  
<213> *Bacillus stearothermophilus*

<400> 177  
atgctggAAC gcgtatgggg aaacattgaa aaacggcgTT tttctccCTt ttatttatta 60  
tacggcaatg agccgtttt attaacggaa acgtatgagc gattggtaa cgcaGcgCTT 120  
ggccccgagg agcgggagtG gaacttggct gtgtacgact gcgaggAAAC gccgatcgAG 180  
gcggcgCTT aggaggCCGA gacggtgCCG ttttcggcg agcggcgTGT cattctcatC 240  
aagcatccat atttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300  
ctggaggcgt acttgaaggc gccgtcgCCG tttcgatcg tcgtttttt cgcGCCgtac 360  
gagaagcttG atgagcgAAA aaaaattacG aagctcgcca aagagcaaAG cgaagtCGTC 420  
atcggcGCCc cgctcgCCGA agcggagCTG cgtgcctggg tgccggcGCCG catcgagAG 480  
caaggggcgc aagcaagcGA cgaggcgATT gatgtcctgt tgccggcggGC cgggacgcAG 540  
cttccgcct tggcgaatga aatcgataAA ttggccctgt ttgcccggatc gggcggAAC 600  
atcgaggcgg cggcggttGA gcccgttGTC gcccgcacGC cggaagaaaaa cgtatttGtG 660  
cttgcgagc aagtggcGA gccgcgacatt ccagcagcgt tgccagacGtt ttatgatctG 720  
cttggaaaaca atgaagagcc gatcaaAAtt ttggcgTTGc tcgcccGCCA tttccgcTTG 780  
cttgcgcaag tgaaatggct tgccctcTTA ggctacggac aggcgcaaat tgctgcggcg 840  
ctcaaggTgc acccgTTccG cgtcaagCTC gctttgCTC aagcggcccG ctTCgCTgac 900  
ggagagcttG ctgaggcgat caacgagCTC gctgacGCCG attacgaAGt gaaaagcGGG 960  
cgccgtcgatc gcccgttggc cgtttagctG cttctgatGc gctggggcgc ccgcccggcg 1020  
caagcggggc gccacggcCG gcgg 1044

<210> 178  
<211> 348  
<212> PRT  
<213> *Bacillus stearothermophilus*

<400> 178  
Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro  
1 5 10 15  
  
Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr  
20 25 30  
  
Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn  
35 40 45  
  
Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu  
50 55 60  
  
Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65

70

75

80

Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His  
85 90 95

Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser  
100 105 110

Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys  
115 120 125

Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro  
130 135 140

Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser  
145 150 155 160

Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg  
165 170 175

Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala  
180 185 190

Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg  
195 200 205

Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln  
210 215 220

Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu  
225 230 235 240

Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala  
245 250 255

His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr  
260 265 270

Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val  
275 280 285

Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala  
290 295 300

Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly  
305 310 315 320

Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg  
340 345

<210> 179

<211> 757

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 179

atgcgatggg aacagctagc gaaacgccag ccgggtggtgg cgaaaatgct gcaaagcgcc 60  
ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacggggcaaa 120  
aaagcggcca gtttgtgtt ggcgaaacgt ttgtttgtc tgcgtccat cggagttcc 180  
ccgtgtctag agtgcgccaa ctgcccggcgc atcgactccg gcaaccaccc tgacgtccgg 240  
gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300  
ttctcgaaaa cagcggtcga gtcggataaa aaaatgtaca tcggttagca cgccgatcaa 360  
atgacgacaa ggcgtgccaa cagccttctg aaattttgg aagagccgca tccggggacg 420  
gtggcggtat tgctgactga gcaataccac cgcctgctag ggacgatcgt ttcccgctgt 480  
caagtgcctt cgttccggcc gttgcccggc gcagagctcg cccagggact tgtcgaggag 540  
cacgtgcgt tgccgttggc gctgttggct gcccatttga caaacagctt cgaggaagca 600  
ctggcgcttg ccaaagatag ttggtttggc gagggcgaa cattagtgtc acaatggtat 660  
gagatgctgg gcaagccgga gctgcagctt ttgttttca tccacgaccg cttgtttccg 720  
catttttgg aaagccatca gcttgacctt ggacttg 757

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met  
1 5 10 15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe  
20 25 30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Ala  
35 40 45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu  
50 55 60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg  
65 70 75 80

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp  
85 90 95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met  
100 105 110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser  
115 120 125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu  
130 135 140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys  
145 150 155 160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly  
165 170 175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His  
180 185 190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp  
195 200 205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly  
210 215 220

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro  
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu  
245 250

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

gtggcataacc aagcgttata tcgcgtgttt cggccgcagc gctttgcgga catggtcggc 60  
caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atgcacgct 120  
tacttatttt ccggcccgcg cggtagcaggaa aaaacgagcg cagcgaaaaat tttcgccaag 180  
gcggtaact gtgaacaggc gcccggcg gagccatgca atgagtgtcc agcttgccctc 240  
ggcattacga atggaacggt tccccatgtc ctggaaaattt acgctgcttc caacaaccgc 300  
gtcgatgaaa ttctgtatcc cggtgagaag gtgaaatttgc cgccaacgtc ggcccgctac 360  
aaagtgtata tcattcgacga ggtgcataatgc ctgtcgatgc gtgcgtttaa cgcgctgttgc 420  
aaaacgttgg aggagccgcc gaaacacgtc attttcattt tggccacgac cgagccgcac 480

aaaattccgg cgacgatcat ttcccgtgc caacggttcg atttcggccg catcccgctt 540  
caggcgatcg tttcacggct aaagtacgtc gcaagcgccc aagggtgtcgaa ggcgtcagat 600  
gaggcattgt ccgcgcattcgca cccgtgtgcga gacggggggta tgccgcgtgc gctcagcttg 660  
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720  
accggggctg catcatttgc cgccttatcg agcttcatcg aagccatcca ccgcaaagat 780  
acagcggcgg ttcttcagca ctggaaacg atgatggcgc aaggaaaga tccgcattcg 840  
ttgggtgaag acttgattt gtactatcg gatttattgc tgtacaaaac cgctccctat 900  
gtggaggggag cgattcaaataat tgctgtcggt gacgaagcgt tcacttcact gtcggaaatg 960  
atccgggttt ccaatttata cgaggccatc gagttgtga acaaaagcca gcaagagatg 1020  
aagtggacaa accaccggcg ccttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080  
tcagccgccc ccccggtcgct gtcggcttcc gagttggAAC cggtgataaa gcggattgaa 1140  
acgctggagg cggaatttgcg ggcgcgtgaag gaacaaccgc ctgccttcc gtcgaccgccc 1200  
gcgcgggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccgggttggc 1260  
cgcatattacg agctgttgaa acaggcgacg catgaagatt tagcttttgtt gaaaggatgc 1320  
tggcggtatg tgctcgacac gttgaaacgg cagcataaag tgctgcacgc tgccttgctg 1380  
caagagagcg agccgggtgc agcgagcgc tcagcgttt tattaaaatt caaatacgaa 1440  
atccactgca aaatggcgac cgatcccaca agttcggtca aagaaaaacgt cgaagcgatt 1500  
ttgttgagc tgacaaaccg cgccttggaa atggtagcca ttccggaggg agaatgggg 1560  
aaaataagag aagagttcat cgcataaag gacccatgg tggaaaaaaag cgaagaagat 1620  
ccgttaatcg ccgaagcgaa gcggctgttt ggcgaagagc tgatcgaaat taaagaa 1677

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

Val	Ala	Tyr	Gln	Ala	Leu	Tyr	Arg	Val	Phe	Arg	Pro	Gln	Arg	Phe	Ala
1					5				10				15		

Asp	Met	Val	Gly	Gln	Glu	His	Val	Thr	Lys	Thr	Leu	Gln	Ser	Ala	Leu
								20		25			30		

Leu	Gln	His	Lys	Ile	Ser	His	Ala	Tyr	Leu	Phe	Ser	Gly	Pro	Arg	Gly
									35		40		45		

Thr	Gly	Lys	Thr	Ser	Ala	Ala	Lys	Ile	Phe	Ala	Lys	Ala	Val	Asn	Cys
								50		55		60			

Glu	Gln	Ala	Pro	Ala	Ala	Glu	Pro	Cys	Asn	Glu	Cys	Pro	Ala	Cys	Leu
								65		70		75		80	

Gly	Ile	Thr	Asn	Gly	Thr	Val	Pro	Asp	Val	Leu	Glu	Ile	Asp	Ala	Ala
								85		90		95			

Ser	Asn	Asn	Arg	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Glu	Lys	Val	Lys
								100		105		110			

Phe Ala Pro Thr Ser Ala Arg Tyr Lys Val Tyr Ile Ile Asp Glu Val  
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu  
130 135 140

Glu Pro Pro Lys His Val Ile Phe Ile Leu Ala Thr Thr Glu Pro His  
145 150 155 160

Lys Ile Pro Ala Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Arg  
165 170 175

Arg Ile Pro Leu Gln Ala Ile Val Ser Arg Leu Lys Tyr Val Ala Ser  
180 185 190

Ala Gln Gly Val Glu Ala Ser Asp Glu Ala Leu Ser Ala Ile Ala Arg  
195 200 205

Ala Ala Asp Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala  
210 215 220

Ile Ser Phe Ser Asp Gly Lys Leu Arg Leu Asp Asp Val Leu Ala Met  
225 230 235 240

Thr Gly Ala Ala Ser Phe Ala Ala Leu Ser Ser Phe Ile Glu Ala Ile  
245 250 255

His Arg Lys Asp Thr Ala Ala Val Leu Gln His Leu Glu Thr Met Met  
260 265 270

Ala Gln Gly Lys Asp Pro His Arg Leu Val Glu Asp Leu Ile Leu Tyr  
275 280 285

Tyr Arg Asp Leu Leu Tyr Lys Thr Ala Pro Tyr Val Glu Gly Ala  
290 295 300

Ile Gln Ile Ala Val Val Asp Glu Ala Phe Thr Ser Leu Ser Glu Met  
305 310 315 320

Ile Pro Val Ser Asn Leu Tyr Glu Ala Ile Glu Leu Leu Asn Lys Ser  
325 330 335

Gln Gln Glu Met Lys Trp Thr Asn His Pro Arg Leu Leu Leu Glu Val  
340 345 350

Ala Leu Val Lys Leu Cys His Pro Ser Ala Ala Ala Pro Ser Leu Ser  
355 360 365

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala  
 370 375 380  
  
 Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala  
 385 390 395 400  
  
 Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys  
 405 410 415  
  
 Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu  
 420 425 430  
  
 Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu  
 435 440 445  
  
 Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu  
 450 455 460  
  
 Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu  
 465 470 475 480  
  
 Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn  
 485 490 495  
  
 Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val  
 500 505 510  
  
 Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg  
 515 520 525  
  
 Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala  
 530 535 540  
  
 Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu  
 545 550 555

<210> 183  
 <211> 4301  
 <212> DNA  
 <213> *Bacillus stearothermophilus*

<400> 183  
 atggtgacaa aagagcaaaa agagcggtt ctcatcctgc ttgagcagct gaagatgacg 60  
 tcggacgaat gcatgccca ttttcgttag gcaggccattc gcaaagtctgt gatcgataaa 120  
 gaggagaaaa gctggcattt ttatttcag ttgcacaacg tgctgccgt tcatagtatac 180  
 aaaacgtttg ccgatcggtt gcagacggcg ttccgcccata tcgccccgtt ccggccatacg 240

atggaggtcg aagcgcgcg cgtaactgag gcggatgtgc aggcgtattg gccgcttgc 300  
cttgcgcagc tgcaagaagg catgtcgccg cttgtcgatt ggctcagccg gcagacgcct 360  
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<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

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20 25 30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr  
 35 40 45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala  
50 55 60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr  
65 70 75 80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr  
85 90 95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val  
100 105 110

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu  
115 120 125

Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe  
130 135 140

Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu  
145 150 155 160

Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe  
165 170 175

Leu Ala Gln Lys Gln Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu  
180 185 190

Thr Asp Leu Ala Arg Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser  
195 200 205

Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg  
210 215 220

Arg Leu Glu Thr Ile Val Glu Glu Glu Arg Arg Val Val Val Gln Gly  
225 230 235 240

Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu  
245 250 255

Leu Thr Met Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met  
260 265 270

Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys  
275 280 285

Gly Met Trp Val Lys Val Arg Gly Ser Val Gln Asn Asp Thr Phe Val  
290 295 300

Arg Asp Leu Val Ile Ile Ala Asn Asp Leu Asn Glu Ile Ala Ala Asn  
305 310 315 320

Glu Arg Gln Asp Thr Ala Pro Glu Gly Glu Lys Arg Val Glu Leu His  
325 330 335

Leu His Thr Pro Met Ser Gln Met Asp Ala Val Thr Ser Val Thr Lys  
340 345 350

Leu Ile Glu Gln Ala Lys Lys Trp Gly His Pro Ala Ile Ala Val Thr  
355 360 365

Asp His Ala Val Val Gln Ser Phe Pro Glu Ala Tyr Ser Ala Ala Lys  
370 375 380

Lys His Gly Met Lys Val Ile Tyr Gly Leu Glu Ala Asn Ile Val Asp  
385 390 395 400

Asp Gly Val Pro Ile Ala Tyr Asn Glu Thr His Arg Arg Leu Ser Glu  
405 410 415

Glu Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val  
420 425 430

Tyr Asn Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Asp Gly Glu  
435 440 445

Ile Ile Asp Arg Phe Met Ser Phe Ala Asn Pro Gly His Pro Leu Ser  
450 455 460

Val Thr Thr Met Glu Leu Thr Gly Ile Thr Asp Glu Met Val Lys Asp  
465 470 475 480

Ala Pro Lys Pro Asp Glu Val Leu Ala Arg Phe Val Asp Trp Ala Gly  
485 490 495

Asp Ala Thr Leu Val Ala His Asn Ala Ser Phe Asp Ile Gly Phe Leu  
500 505 510

Asn Ala Gly Leu Ala Arg Met Gly Arg Gly Lys Ile Ala Asn Pro Val  
515 520 525

Ile Asp Thr Leu Glu Leu Ala Arg Phe Leu Tyr Pro Asp Leu Lys Asn  
530 535 540

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln  
545 550 555 560

His His Arg Ala Ile Tyr Asp Ala Glu Ala Thr Gly His Leu Leu Met  
565 570 575

Arg Leu Leu Lys Glu Ala Glu Glu Arg Gly Ile Leu Phe His Asp Glu  
580 585 590

Leu Asn Ser Arg Thr His Ser Glu Ala Ser Tyr Arg Leu Ala Arg Pro  
595 600 605

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu  
610 615 620

Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro  
625 630 635 640

Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val  
645 650 655

Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys  
660 665 670

Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu  
675 680 685

Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val  
690 695 700

Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu  
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Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr  
725 730 735

Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln  
740 745 750

Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe  
755 760 765

Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu  
770 775 780

Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu  
785 790 795 800

Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile  
805 810 815

Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys  
820 825 830

Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu  
835 840 845

Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu  
850 855 860

Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val  
865 870 875 880

Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu  
885 890 895

Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys  
900 905 910

Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp  
915 920 925

Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp  
930 935 940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys  
945 950 955 960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala  
965 970 975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala  
980 985 990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys  
995 1000 1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp  
1010 1015 1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro  
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Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr  
1045 1050 1055

Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr  
1060 1065 1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile  
1075 1080 1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser  
1090 1095 1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly  
1105 1110 1115 1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met  
1125 1130 1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val  
1140 1145 1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val  
1155 1160 1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala  
1170 1175 1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly  
1185 1190 1195 1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro  
1205 1210 1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu  
1220 1225 1230

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp  
1235 1240 1245

Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His  
1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val  
1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu  
1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys  
1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu  
1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg  
1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu  
1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro  
1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu  
1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser  
 1395 1400 1405  
  
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 Pro Asp His Asn Gln Leu Ser Leu Phe  
 1425 1430  
  
<210> 185  
<211> 199  
<212> PRT  
<213> Thermus thermophilus  
  
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Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser  
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Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala  
35 40 45  
  
Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala  
50 55 60  
  
Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu  
65 70 75 80  
  
Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu  
85 90 95  
  
Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala  
100 105 110  
  
Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys  
115 120 125  
  
Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys  
130 135 140  
  
Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu  
145 150 155 160  
  
Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro  
180 185 190

Ala Gly Gln Pro Arg Val Asp  
195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccagtacc tcgcctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gctttctcggt cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggagcg ggagctggag aagcttgcac tcctctcccc acccctcacc 60  
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cgctccgtcc tggagaagga ccccaaggag gcccctcgc gcctcaggcg cctcagggag 180  
gagggggagg agccctcag gtcctcggt gcccctcctt ggcagttcgc ctcctcgcc 240  
cgggccttct tcctcctccg gaaaaacccc aggcccaagg aggaggaccc cgcccgcc 300  
gaggcccacc cctacgccgc caagaaggcc a 331

<210> 189

<211> 110

<212> PRT

<213> Thermus thermophilus

<400> 189

Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser  
1 5 10 15

Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro  
20 25 30

Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro  
35 40 45

Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu  
50 55 60

Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala  
65 70 75 80

Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp  
85 90 95

Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala  
100 105 110

<210> 190

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 190

gtggtgtcta gacatcataa cggttctggc a

31

<210> 191

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 191

gaggggccacc accttctcca ccttctc

27

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 192  
ctccgtcctg gagaaggacc ccaag

25

<210> 193  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<220>  
<221> primer\_bind  
<222> (15)  
<223> S at position 15 can be either C or G

<220>  
<221> primer\_bind  
<222> (27)  
<223> S at position 27 can be either C or G

<400> 193  
cgcgaattca acgcsctcct caagacsct

29

<210> 194  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 194  
gacacttaac atatggtcat cgcccttcacc g

31

<210> 195  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 195  
gttgtgaat tcgggtcaac gggcgaggcg gaggaccg 38

<210> 196  
<211> 10  
<212> PRT  
<213> Deinococcus radiodurans

<400> 196  
Val Ile Leu Asn Pro Gly Ser Val Gly Gln  
1 5 10

<210> 197  
<211> 10  
<212> PRT  
<213> Methanococcus jannaschii

<400> 197  
Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln  
1 5 10

<210> 198  
<211> 10  
<212> PRT  
<213> Thermotoga maritima

<400> 198  
Leu Val Leu Asn Pro Gly Ser Ala Gly Arg  
1 5 10

<210> 199  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 199  
ctggtaacc cgggctccgt gggccagc

28

<210> 200  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 200  
Leu Leu Val Asn Pro Gly Ser Val Gly Gln  
1 5 10

<210> 201  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 201  
ctcgaggagc ttgaggaggg tgttggc

27

<210> 202  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 202  
Ala Asn Thr Leu Leu Lys Leu Leu Glu  
1 5

<210> 203  
<211> 32  
<212> PRT

<213> Deinococcus radiodurans

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly  
20 25 30

<210> 204

<211> 32

<212> PRT

<213> Caenorhabditis elegans

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly  
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<210> 205

<211> 32

<212> PRT

<213> Pseudomonas aeruginosa

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser  
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly  
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser  
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Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly  
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<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr

1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccg cgtggagctc cac 33

<210> 210  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: polypeptide

<400> 210  
Val Glu Leu His Ala Ala His Gly Tyr Leu Leu  
1 5 10

<210> 211  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 211  
ggctttccca tatggctcta cacccggctc ac 32

<210> 212  
<211> 29  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR primer

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